GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:02:07 ; Search time 16.5871 Seconds
(without alignments)
3219.466 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	925	100.0	361	3	AAY71385	Aay71385 Alternati
2	925	100.0	1163	3	AAY71310	Aay71310 Rat neuri
3	925	100.0	1163	3	AAY71384	Aay71384 Alternati
4	925	100.0	1163	5	ABB81074	Abb81074 Rat neuro
5	922	99.7	379	7	ADB85283	Adb85283 Rat fooce
6	921	99.6	199	5	ABB81077	Abb81077 Rat neuro
7	921	99.6	360	3	AAY71383	Aay71383 Rat neuri
8	921	99.6	360	5	ABB81076	Abb81076 Rat neuro
9	921	99.6	522	3	AAY71312	Aay71312 Rat neuri

10	919	99.4	199	3	AAY71559	Aay71559 Rat Nogo
11	919	99.4	359	3	AAY71558	Aay71558 Rat Nogo
12	919	99.4	403	3	AAY71563	Aay71563 Rat Nogo
13	919	99.4	1162	3	AAY71557	Aay71557 Rat Nogo
14	908	98.2	893	3	AAY95012	Aay95012 Human sec
15	908	98.2	983	6	ABU11573	Abu11573 Human MDD
16	908	98.2	1178	3	AAY71311	Aay71311 Human neu
17	908	98.2	1192	3	AAY56967	Aay56967 Human MAG
18	908	98.2	1192	4	AAB82349	Aab82349 Human NOG
19	908	98.2	1192	4	AAU04591	Aau04591 Human Nog
20	908	98.2	1192	5	ABG30938	Abg30938 Human Nog
21	908	98.2	1192	5	ABP68600	Abp68600 Human pan
22	908	98.2	1192	5	ABB81078	Abb81078 Human neu
23	908	98.2	1192	6	ABR59667	Abr59667 Human Nog
24	905	97.8	200	4	AAB64514	Aab64514 Human sec
25	904	97.7	199	2	AAW53947	Aaw53947 Human NSP
26	904	97.7	199	2	AAW78313	Aaw78313 Fragment
27	904	97.7	199	3	AAB12805	Aab12805 Human NSP
28	904	97.7	199	4	AAB82348	Aab82348 Human NOG
29	904	97.7	199	5	ABB81080	Abb81080 Human neu
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31	904	97.7	373	3	AAY56969	Aay56969 Human MAG
32	904	97.7	373	3	AAB24242	Aab24242 Human Nog
33	904	97.7	373	4	AAB82350	Aab82350 Human NOG
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35	904	97.7	373	5	ABG30937	Abg30937 Human Nog
36	904	97.7	373	5	ABP68601	Abp68601 Human pan
37	904	97.7	373	5	ABB81079	Abb81079 Human neu
38	900	97.3	291	4	AAM93484	Aam93484 Human pol
39	895	96.8	199	2	AAY35903	Aay35903 Extended
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41	871.5	94.2	642	4	AAB90682	Aab90682 Human BG1
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ALIGNMENTS

RESULT 1
AAY71385
ID AAY71385 standard; protein; 361 AA.
XX
AC AAY71385;
XX
DT 02-NOV-2000 (first entry)
XX
DE Alternative version of rat neurite growth inhibitor Nogo B.
XX
KW Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Region 1. .172
FT /note= "Corresponds to amino acids 1-172 of Nogo A
FT protein shown in AAY71310"
FT Inhibitory-site 1. .171
FT /note= "Inhibits NIH 3T3 fibroblast spreading"
FT Modified-site 30
FT /note= "Casein kinase II site"
FT Region 31. .58
FT /note= "Acidic region"
FT Region 173. .361
FT /note= "Corresponds to amino acids 975-1163 of Nogo A
FT protein (AAY71310)"
FT Region 174. .361
FT /note= "This region is common to Nogo A, B and C
FT isoforms"
FT Domain 186. .221
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FT /note= "C-terminal hydrophobic region"
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FT /note= "Asn is N-glycosylated"
FT Modified-site 271
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 287
FT /note= "Protein kinase C (PKC) site"
FT Domain 288. .323
FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 339. .341
FT /note= "Asn is N-glycosylated"
FT Modified-site 341
FT /note= "Protein kinase C (PKC) site"
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PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX

PS Claim 4; Page; 122pp; English.
XX
CC The present sequence is an alternative version of rat Nogo B protein
CC which is a potent neural cell growth inhibitor and is free of all central
CC nervous system (CNS) myelin material with which it is natively
CC associated. The Nogo B transcript arises as a result of alternative
CC splicing of Nogo gene. Nogo proteins and fragments displaying neurite
CC growth inhibitory activity are used in the treatment of neoplastic
CC disease of the CNS e.g. glioma, glioblastoma, medulloblastoma,
CC craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic
CC neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma
CC and degenerative nerve diseases e.g. Alzheimer's and Parkinson's
CC diseases. Therapeutics which promote Nogo activity can be used to treat
CC or prevent hyperproliferative or benign dysproliferative disorders e.g.
CC psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic
CC acids can be used to inhibit production of Nogo protein to induce
CC regeneration of neurons or to promote structural plasticity of the CNS in
CC disorders where neurite growth, regeneration or maintenance are deficient
CC or desired. The animal models can be used in diagnostic and screening
CC methods for predisposition to disorders and to screen for or test
CC molecules which can treat or prevent disorders or diseases of the CNS.
CC Note: The present sequence is not given in the specification but is
CC derived from Nogo A protein sequence (AAY71310) and corresponds to
CC residues 1-172 fused to 975-1163 of Nogo A. This sequence is an
CC alternative version of the Nogo B sequence (see AAY71383) described in
CC the specification as being residues 1-172 fused to C-terminal 188 amino
CC acids (residues 976-1163) of Nogo A. SEQ ID numbers 35-42 are referred in
CC claim 32 and SEQ ID NO: 29 in disclosure of the specification. However
CC the specification does not include sequences for these SEQ ID numbers
XX
SQ Sequence 361 AA;

Query Match 100.0%; Score 925; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.7e-90;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        181 IPGLKRKAD 189
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Db        353 IPGLKRKAD 361
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RESULT 2
AAY71310
ID AAY71310 standard; protein; 1163 AA.
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AC AAY71310;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat neurite growth inhibitor Nogo A.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
OS Rattus sp.
XX

FH	Key	Location/Qualifiers
FT	Inhibitory-site	1. .171
FT		/note= "Inhibits NIH 3T3 fibroblast spreading"
FT	Modified-site	30
FT		/note= "Casein kinase II site"
FT	Region	31. .58
FT		/note= "Acidic region"
FT	Region	31. .57
FT		/note= "Region specifically described in claim 16"
FT	Region	172. .259
FT		/note= "This region is not essential for inhibitory
FT		activity"
FT	Modified-site	233
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	242. .244
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	291
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	295
FT		/note= "Protein kinase C (PKC) site"
FT	Misc-difference	404
FT		/note= "Encoded by TTG"
FT	Modified-site	436
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	468. .470
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	484
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FT	Modified-site	502
FT		/note= "Casein kinase II site"
FT	Inhibitory-site	542. .722
FT	Modified-site	576
FT		/note= "Casein kinase II site"
FT	Peptide	623. .640
FT		/note= "used as immunogen to generate antibody AS 472"
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FT		/note= "Asn is N-glycosylated"

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FT   Peptide         762. .1163
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FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   863
FT                   /note= "Casein kinase II site"
FT   Modified-site   868
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   893
FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   912. .914
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   925. .927
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   954
FT                   /note= "PKC and casein kinase II sites"
FT   Modified-site   956
FT                   /note= "PKC and casein kinase II sites"
FT   Region          975. .1162
FT                   /note= "This region is not essential for inhibitory
FT                   activity"
FT   Region          976. .1163
FT                   /note= "C-terminal common region found in Nogo A, B and C
FT                   isoforms"
FT   Domain          988. .1023
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FT                   /note= "C-terminal hydrophobic region specifically
FT                   described in claim 16"
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FT                   /note= "Protein kinase C (PKC) site"
FT   Modified-site   1071. .1073
FT                   /note= "Asn is N-glycosylated"
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FT                   /note= "Protein kinase C (PKC) site"
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
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PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
DR N-PSDB; AAD01173.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 3; Fig 2A; 122pp; English.
XX
CC The present sequence is a rat Nogo A protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The protein was
CC derived from a cDNA generated by fusing RO18U37-3, R1-3U21 cDNAs isolated
CC from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18
CC cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins
CC and fragments displaying neurite growth inhibitory activity are used in
CC the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 1163 AA;

Query Match 100.0%; Score 925; DB 3; Length 1163;
Best Local Similarity 100.0%; Pred. No. 4e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Qy 61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
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Qy        181 IPGLKRKAD 189
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RESULT 3
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ID AAY71384 standard; protein; 1163 AA.
XX
AC AAY71384;
XX
DT 02-NOV-2000 (first entry)
XX
DE Alternative version of rat neurite growth inhibitor Nogo A.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.
XX
OS Rattus sp.
XX

FH	Key	Location/Qualifiers
FT	Inhibitory-site	1. .171
FT		/note= "Inhibits NIH 3T3 fibroblast spreading"
FT	Modified-site	30
FT		/note= "Casein kinase II site"
FT	Region	31. .58
FT		/note= "Acidic region"
FT	Region	172. .259
FT		/note= "This region is not essential for inhibitory
FT		activity"
FT	Misc-difference	223
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FT		/note= "There is Leu at this position in the sequence
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FT	Modified-site	233
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	242. .244
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	291
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	295
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FT	Misc-difference	404
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FT		shown in AAY71310"
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FT                   /note= "Asn is N-glycosylated"
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FT   Modified-site   484
FT                   /note= "Protein kinase C (PKC) site"
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FT                   /note= "Casein kinase II site"
FT   Inhibitory-site 542. .722
FT   Modified-site   576
FT                   /note= "Casein kinase II site"
FT   Peptide         623. .640
FT                   /note= "used as immunogen to generate antibody AS 472"
FT   Modified-site   626
FT                   /note= "Protein kinase C (PKC) site"
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FT   Modified-site   715
FT                   /note= "Casein kinase II site"
FT   Peptide         762. .1163
FT                   /note= "used as immunogen to generate antibody AS Bruna"
FT   Modified-site   784
FT                   /note= "Protein kinase C (PKC) site"
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FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   954
FT                   /note= "PKC and casein kinase II sites"
FT   Modified-site   956
FT                   /note= "PKC and casein kinase II sites"
FT   Region          975. .1162
FT                   /note= "This region is not essential for inhibitory
FT                   activity"
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FT Region 976. .1163
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FT /note= "C-terminal hydrophobic region"
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PN WO200031235-A2.
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PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 3; Fig 13; 122pp; English.
XX
CC The present sequence is an alternative version of rat Nogo A protein
CC which is a potent neural cell growth inhibitor and is free of all central
CC nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The

```
CC   animal models can be used in diagnostic and screening methods for
CC   predisposition to disorders and to screen for or test molecules which can
CC   treat or prevent disorders or diseases of the CNS. Note: The present
CC   sequence is an alternative version of the Nogo A sequence shown in Fig.
CC   2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ
CC   ID NO: 29 in disclosure of the specification. However the specification
CC   does not include sequences for these SEQ ID numbers
XX
SQ   Sequence 1163 AA;

  Query Match             100.0%;  Score 925;  DB 3;  Length 1163;
  Best Local Similarity   100.0%;  Pred. No. 4e-89;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154

Qy        181 IPGLKRKAD 189
              |||||||||
Db       1155 IPGLKRKAD 1163


RESULT 4
ABB81074
ID   ABB81074 standard; protein; 1163 AA.
XX
AC   ABB81074;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Rat neurotransmitter receptor protein Nogo-A.
XX
KW   Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW   central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW   vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW   nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW   osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW   neurotransmitter receptor; rat; receptor.
XX
OS   Rattus norvegicus.
XX
PN   US2002072493-A1.
XX
PD   13-JUN-2002.
XX
PF   28-JUN-2001; 2001US-00893348.
XX
PR   19-MAY-1998;   98IL-00124500.
```

PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR N-PSDB; ABN86600.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Example 5; Page 44-47; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
CC antigen
XX
SQ Sequence 1163 AA;

Query Match 100.0%; Score 925; DB 5; Length 1163;
Best Local Similarity 100.0%; Pred. No. 4e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60

```
Db        975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154

Qy        181 IPGLKRKAD 189
              |||||||||
Db       1155 IPGLKRKAD 1163
```

RESULT 5
ADB85283
ID ADB85283 standard; protein; 379 AA.
XX
AC ADB85283;
XX
DT 04-DEC-2003 (first entry)
XX
DE Rat foocen-m2 reticulon SEQ ID NO:164.
XX
KW rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;
KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;
KW protease; enzyme; analgesic; gene therapy; pain; diabetes.
XX
OS Rattus norvegicus.
XX
PN EP1284297-A2.
XX
PD 19-FEB-2003.
XX
PF 26-JUL-2002; 2002EP-00255228.
XX
PR 27-JUL-2001; 2001GB-00018354.
PR 07-FEB-2002; 2002GB-00002880.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
XX
DR WPI; 2003-364994/35.
DR N-PSDB; ADB85284.
XX
PT Use of gene sequence that is down-regulated in response to streptozocin-
PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in
PT screening of compounds for treating or diagnosing pain.
XX
PS Disclosure; Page 239-240; 256pp; English.
XX
CC The invention relates to a novel isolated gene sequence that is down-
CC regulated in the spinal cord in response to streptozocin-induced
CC diabetes, or comprising, hybridising or having at least 80% sequence
CC identity to a sequence whose expression products are kinases,

CC phosphatases, ion channel proteins, receptors, transporters, G-protein
CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,
CC given in the specification. A gene of the invention has analgesic
CC activity, and may have a use in gene therapy. The gene sequences, vector,
CC host cell, animal, polypeptide and antibody are useful for screening of
CC compounds for diagnosing or treating pain. The kits are useful for
CC simultaneous, separate or sequential detecting and/or quantifying down-
CC regulation of a gene sequence in the spinal cord of a mammal in response
CC to streptozocin-induced diabetes. The compound or pharmaceutical
CC composition is useful as a medicament for treating or diagnosing pain.
CC The present sequence represents a protein encoded by a gene of the
CC invention.
XX
SQ Sequence 379 AA;

Query Match 99.7%; Score 922; DB 7; Length 379;
Best Local Similarity 99.5%; Pred. No. 1.9e-89;
Matches 188; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 250

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 310

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 370

Qy        181 IPGLKRKAD 189
              |||||||||
Db        371 IPGLKRKAD 379
```

RESULT 6
ABB81077
ID ABB81077 standard; protein; 199 AA.
XX
AC ABB81077;
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat neurotransmitter receptor protein Nogo-C.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.
XX
OS Rattus norvegicus.
XX
PN US2002072493-A1.
XX

PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR N-PSDB; ABN86600.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Example 5; Page 48-49; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-C, an example of NS-specific
CC antigen
XX
SQ Sequence 199 AA;

Query Match 99.6%; Score 921; DB 5; Length 199;

```
  Best Local Similarity   100.0%;  Pred. No. 1.1e-89;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 191

Qy        182 PGLKRKAD 189
              ||||||||
Db        192 PGLKRKAD 199


RESULT 7
AAY71383
ID   AAY71383 standard; protein; 360 AA.
XX
AC   AAY71383;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat neurite growth inhibitor Nogo B.
XX
KW   Rat; neurite growth inhibitor; Nogo B; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .172
FT                   /note= "Corresponds to amino acids 1-172 of Nogo A
FT                   protein shown in AAY71310"
FT   Inhibitory-site 1. .171
FT                   /note= "Inhibits NIH 3T3 fibroblast spreading"
FT   Modified-site   30
FT                   /note= "Casein kinase II site"
FT   Region          31. .58
FT                   /note= "Acidic region"
FT   Region          173. .360
FT                   /note= "Corresponds to C-terminal 188 amino acids
FT                   (residues 976-1163) of Nogo A protein (AAY71310). This
FT                   region is common to Nogo A, B and C isoforms"
FT   Domain          185. .220
FT                   /label= Transmembrane_domain
FT                   /note= "C-terminal hydrophobic region"
```

FT Modified-site 221
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 268. .270
FT /note= "Asn is N-glycosylated"
FT Modified-site 270
FT /note= "Protein kinase C (PKC) site"
FT Modified-site 286
FT /note= "Protein kinase C (PKC) site"
FT Domain 287. .322
FT /label= Transmembrane_domain
FT /note= "C-terminal hydrophobic region"
FT Modified-site 338. .340
FT /note= "Asn is N-glycosylated"
FT Modified-site 340
FT /note= "Protein kinase C (PKC) site"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The present sequence is a rat Nogo B protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The Nogo B
CC transcript arises as a result of alternative splicing of Nogo gene. Nogo
CC proteins and fragments displaying neurite growth inhibitory activity are
CC used in the treatment of neoplastic disease of the CNS e.g. glioma,
CC glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence is
CC not given in the specification but is derived from Nogo A protein
CC sequence (AAY71310) and corresponds to residues 1-172 fused to 976-1163

CC of Nogo A. The specification claims an alternative version of this
CC sequence (see AAY71385.) which corresponds to residues 1-172 fused to 975
CC -1163 of Nogo A. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID
CC NO: 29 in disclosure of the specification. However the specification does
CC not include sequences for these SEQ ID numbers
XX
SQ Sequence 360 AA;

Query Match 99.6%; Score 921; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 232

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 292

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352

Qy        182 PGLKRKAD 189
              ||||||||
Db        353 PGLKRKAD 360
```

RESULT 8
ABB81076
ID ABB81076 standard; protein; 360 AA.
XX
AC ABB81076;
XX
DT 05-NOV-2002 (first entry)
XX
DE Rat neurotransmitter receptor protein Nogo-B.
XX
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; rat; receptor.
XX
OS Rattus norvegicus.
XX
PN US2002072493-A1.
XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR N-PSDB; ABN86600.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Example 5; Page 47-48; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents the rat
CC neurotransmitter receptor protein Nogo-B, an example of NS-specific
CC antigen
XX
SQ Sequence 360 AA;

Query Match 99.6%; Score 921; DB 5; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 232

```
Qy          62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 292

Qy         122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         293 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352

Qy         182 PGLKRKAD 189
               ||||||||
Db         353 PGLKRKAD 360
```

```
RESULT 9
AAY71312
ID   AAY71312 standard; protein; 522 AA.
XX
AC   AAY71312;
XX
DT   02-NOV-2000  (first entry)
XX
DE   Rat neurite growth inhibitor Nogo C.
XX
KW   Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;
KW   central nervous system; neoplastic disease; antiproliferative; glioma;
KW   antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW   degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW   hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW   psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW   structural plasticity; screening.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .39
FT                   /note= "Sequence upstream to the N-terminus of Nogo C
FT                   protein"
FT   Misc-difference 3
FT                   /note= "Encoded by TAG"
FT   Region          11. .191
FT                   /note= "Region specifically described in claim 16"
FT   Misc-difference 29
FT                   /note= "Encoded by TAA"
FT   Protein         40. .238
FT                   /label= Nogo_C_protein
FT   Region          51. .238
FT                   /note= "C-terminal common region found in Nogo A, B and C
FT                   isoforms "
FT   Region          239. .522
FT                   /note= "Sequence downstream to the C-terminus of Nogo C
FT                   protein"
FT   Misc-difference 239
FT                   /note= "Encoded by TGA"
FT   Misc-difference 263
FT                   /note= "Encoded by TGA"
FT   Misc-difference 276
FT                   /note= "Encoded by TAG"
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FT   Misc-difference 281
FT                   /note= "Encoded by TGA"
FT   Misc-difference 295
FT                   /note= "Encoded by TAA"
FT   Misc-difference 298
FT                   /note= "Encoded by TAA"
FT   Misc-difference 314
FT                   /note= "Encoded by TGA"
FT   Misc-difference 318
FT                   /note= "Encoded by TGA"
FT   Misc-difference 335
FT                   /note= "Encoded by TAG"
FT   Misc-difference 371
FT                   /note= "Encoded by TGA"
FT   Misc-difference 374
FT                   /note= "Encoded by TAG"
FT   Misc-difference 380
FT                   /note= "Encoded by TAA"
FT   Misc-difference 406
FT                   /note= "Encoded by TAA"
FT   Misc-difference 408
FT                   /note= "Encoded by TAG"
FT   Misc-difference 410
FT                   /note= "Encoded by TAA"
FT   Misc-difference 422
FT                   /note= "Encoded by TAA"
FT   Misc-difference 433
FT                   /note= "Encoded by TGA"
FT   Misc-difference 440
FT                   /note= "Encoded by TAG"
FT   Misc-difference 453
FT                   /note= "Encoded by TAG"
FT   Misc-difference 465
FT                   /note= "Encoded by TAG"
FT   Misc-difference 482
FT                   /note= "Encoded by TAG"
FT   Misc-difference 513
FT                   /note= "Encoded by TAA"
XX
PN   WO200031235-A2.
XX
PD   02-JUN-2000.
XX
PF   05-NOV-1999;    99WO-US026160.
XX
PR   06-NOV-1998;    98US-0107446P.
XX
PA   (SCHW/) SCHWAB M E.
PA   (CHEN/) CHEN M S.
XX
PI   Schwab ME,  Chen MS;
XX
DR   WPI; 2000-400052/34.
DR   N-PSDB; AAD01175.
XX
PT   Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT   of the central nervous system and inducing regeneration of neurons.
```

XX
PS Claim 7; Fig 14; 122pp; English.
XX
CC The present sequence is a rat Nogo C protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. Nogo proteins and
CC fragments displaying neurite growth inhibitory activity are used in the
CC treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 522 AA;

Query Match 99.6%; Score 921; DB 3; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 110

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 170

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 230

Qy        182 PGLKRKAD 189
              ||||||||
Db        231 PGLKRKAD 238
```

RESULT 10
AAY71559
ID AAY71559 standard; protein; 199 AA.
XX
AC AAY71559;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C.

XX
KW Rat; neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Region 1. .11
FT /note= "Corresponds to residues 40-50 of rat Nogo C
FT protein shown in AAY71312"
FT Region 12. .199
FT /note= "Corresponds to residues 975-1162 of rat Nogo A
FT protein shown in AAY71310"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is derived by fusing two fragments from rat Nogo C and Nogo A proteins.

CC The fragment is used in the construction of mutant Nogo-C which is
CC composed of His-tag/T7-tag/Nogo-C N-terminus (11 aa) + Nogo-A sequence aa
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In
CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC fibroblast spreading. Note: The present sequence is not given in the
CC specification but is derived from rat Nogo C sequence shown in AAY71312
CC and Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
SQ Sequence 199 AA;

Query Match 99.4%; Score 919; DB 3; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 71

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 131

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 191

Qy        181 IPGLKRKA 188
              ||||||||
Db        192 IPGLKRKA 199
```

RESULT 11
AAY71558
ID AAY71558 standard; protein; 359 AA.
XX
AC AAY71558;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo A protein fragment used in the construction of mutant Nogo-B.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers

FT Region 1. .171
FT /note= "Corresponds to residues 1-171 of rat Nogo A
FT protein shown in AAY71310"
FT Region 172. .359
FT /note= "Corresponds to residues 975-1162 of rat Nogo A
FT protein shown in AAY71310"
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is derived by fusing two fragments of rat Nogo A protein shown in
CC AAY71310. The fragment is used in the construction of mutant Nogo-B. The
CC mutant is composed of His-tag/T7-tag/vector/Nogo-A sequence aa 1-171 +
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In
CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3
CC fibroblast spreading. Note: The present sequence is not given in the
CC specification but is derived from rat Nogo A sequence shown in AAY71310.
CC SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in
CC disclosure of the specification. However, the specification does not
CC include sequences for these SEQ ID numbers
XX

SQ Sequence 359 AA;

Query Match 99.4%; Score 919; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 3.8e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 231

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 291

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 351

Qy        181 IPGLKRKA 188
              ||||||||
Db        352 IPGLKRKA 359
```

RESULT 12
AAY71563
ID AAY71563 standard; protein; 403 AA.
XX
AC AAY71563;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo A protein fragment used in the construction of mutant EST.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.

XX

PS Example; Page; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in
CC the construction of mutant EST. The mutant is composed of His-tag/T7-
CC tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for
CC mapping the inhibitory sites of Nogo protein. Major inhibitory region was
CC identified in the Nogo A sequence from amino acids 172-974, particularly
CC amino acids 542-722. In addition, N-terminal region 1-171 was found to be
CC inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is
CC not given in the specification but is derived from rat Nogo A sequence
CC shown in AAY71310. SEQ ID numbers 35-42 are referred in claim 32 and SEQ
CC ID NO: 29 in disclosure of the specification. However, the specification
CC does not include sequences for these SEQ ID numbers

XX

SQ Sequence 403 AA;

Query Match 99.4%; Score 919; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 4.4e-89;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 275

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 335

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 395

Qy        181 IPGLKRKA 188
              ||||||||
Db        396 IPGLKRKA 403
```

RESULT 13
AAY71557
ID AAY71557 standard; protein; 1162 AA.
XX
AC AAY71557;
XX
DT 02-NOV-2000 (first entry)
XX
DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
XX
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening; mutant; mutein.
XX
OS Rattus sp.
XX
PN WO200031235-A2.
XX
PD 02-JUN-2000.
XX
PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Example; Page; 122pp; English.
XX
CC The patent relates to neurite growth inhibitor Nogo which is free of all
CC central nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can

CC treat or prevent disorders or diseases of the CNS. The present sequence
CC is a truncated form of rat Nogo A protein shown in AAY71310, which is
CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-
CC tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were
CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
CC region was identified in the Nogo A sequence from amino acids 172-974,
CC particularly amino acids 542-722. In addition, N-terminal region 1-171
CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers
XX
SQ Sequence 1162 AA;

Query Match 99.4%; Score 919; DB 3; Length 1162;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154

Qy        181 IPGLKRKA 188
              ||||||||
Db       1155 IPGLKRKA 1162
```

RESULT 14
AAY95012
ID AAY95012 standard; protein; 893 AA.
XX
AC AAY95012;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human secreted protein vb22_1, SEQ ID NO:64.
XX
KW Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200011015-A1.
XX
PD 02-MAR-2000.

XX
PF 24-AUG-1999; 99WO-US019351.
XX
PR 24-AUG-1998; 98US-0097638P.
PR 24-AUG-1998; 98US-0097659P.
PR 09-SEP-1998; 98US-0099618P.
PR 28-SEP-1998; 98US-0102092P.
PR 25-NOV-1998; 98US-0109978P.
PR 23-DEC-1998; 98US-0113645P.
PR 23-DEC-1998; 98US-0113646P.
PR 23-AUG-1999; 99US-00379246.
XX
PA (ALPH-) ALPHAGENE INC.
XX
PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
XX
DR WPI; 2000-224657/19.
XX
PT New secreted or transmembrane proteins and polynucleotides encoding them,
PT useful for treating neurodegenerative disorders, autoimmune diseases and
PT cancer.
XX
PS Claim 73; Page 322-325; 357pp; English.
XX
CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
CC of the invention include those that are thought to be only partially
CC secreted, i.e., transmembrane proteins. The proteins of the invention may
CC exhibit one or more activities selected from the following: cytokine
CC activity; cell proliferation; differentiation; immune modulation;
CC haematopoiesis regulation; tissue growth activity; activin/inhibin
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; anti-inflammatory activity; and tumour inhibition activity. The
CC proteins may be administered to patients as vaccines, and the nucleotides
CC may be used as part of a gene therapy regime. Diseases or conditions that
CC may be treated using the proteins or nucleotides of the invention include
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and
CC allergic reactions such as asthma and anaemia. They may also be used for
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
CC activity may additionally be useful as contraceptives. Nucleic acid
CC sequences of the invention may be used in chromosome mapping, and as a
CC source of diagnostic primers and probes. The present sequence represents
CC one of the 40 proteins of the invention
XX
SQ Sequence 893 AA;

Query Match 98.2%; Score 908; DB 3; Length 893;
Best Local Similarity 97.4%; Pred. No. 1.8e-87;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60


```
Db        705 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 764

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        765 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 824

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db        825 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 884

Qy        181 IPGLKRKAD 189
              ||||||||:
Db        885 IPGLKRKAE 893
```

```
RESULT 15
ABU11573
ID   ABU11573 standard; protein; 983 AA.
XX
AC   ABU11573;
XX
DT   12-FEB-2003  (first entry)
XX
DE   Human MDDT polypeptide SEQ ID 520.
XX
KW   MDDT; human; disease detection and treatment molecule polypeptide;
KW   anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
KW   haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
KW   gene therapy; protein replacement therapy; cell proliferative disorder;
KW   cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
KW   anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
KW   Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
KW   psoriasis; hepatitis.
XX
OS   Homo sapiens.
XX
PN   WO200279449-A2.
XX
PD   10-OCT-2002.
XX
PF   27-MAR-2002; 2002WO-US009944.
XX
PR   28-MAR-2001; 2001US-0279619P.
PR   29-MAR-2001; 2001US-0280067P.
PR   29-MAR-2001; 2001US-0280068P.
PR   16-MAY-2001; 2001US-0291280P.
PR   17-MAY-2001; 2001US-0291829P.
PR   17-MAY-2001; 2001US-0291849P.
PR   19-JUN-2001; 2001US-0299428P.
PR   20-JUN-2001; 2001US-0299776P.
PR   20-JUN-2001; 2001US-0300001P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Daffo A,  Jones AL,  Tran AB,  Dahl CR,  Gietzen D,  Chinn J;
PI   Dufour GE,  Hillman JL,  Yu JY,  Tuason O,  Yap PE,  Amshey SR;
PI   Daugherty SC,  Dam TC,  Liu TF,  Nguyen DA,  Kleefeld Y,  Gerstin EH;
```

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-058431/05.
DR N-PSDB; ABX34563.
XX
PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.
XX
PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.
XX
CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 983 AA;

Query Match 98.2%; Score 908; DB 6; Length 983;
Best Local Similarity 97.4%; Pred. No. 2.1e-87;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        795 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 854

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
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Db        855 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 914

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
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Qy        181 IPGLKRKAD 189
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Db        975 IPGLKRKAE 983
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Search completed: September 29, 2004, 18:13:55
Job time : 17.5871 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:09:33 ; Search time 4.69196 Seconds
(without alignments)
2079.581 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	904	97.7	199	2	US-08-700-607-1	Sequence 1, Appli
2	679	73.4	208	2	US-08-700-607-7	Sequence 7, Appli
3	679	73.4	356	2	US-08-700-607-6	Sequence 6, Appli
4	679	73.4	776	2	US-08-700-607-5	Sequence 5, Appli
5	665	71.9	267	2	US-08-700-607-8	Sequence 8, Appli
6	539.5	58.3	168	4	US-09-149-476-563	Sequence 563, App
7	516	55.8	241	2	US-08-700-607-3	Sequence 3, Appli
8	286	30.9	92	4	US-09-149-476-411	Sequence 411, App
9	100	10.8	80	3	US-08-905-223-411	Sequence 411, App
10	95	10.3	468	4	US-08-487-596-8	Sequence 8, Appli
11	95	10.3	468	4	US-08-660-451A-8	Sequence 8, Appli

12	88.5	9.6	1278	4	US-09-462-136-2	Sequence 2, Appli
13	86.5	9.4	592	4	US-09-134-000C-5477	Sequence 5477, Ap
14	86	9.3	414	4	US-08-956-171E-5246	Sequence 5246, Ap
15	85.5	9.2	1051	4	US-09-134-001C-5005	Sequence 5005, Ap
16	84.5	9.1	593	4	US-09-328-352-4866	Sequence 4866, Ap
17	82	8.9	614	4	US-09-540-236-2858	Sequence 2858, Ap
18	81.5	8.8	280	4	US-09-543-681A-6175	Sequence 6175, Ap
19	81	8.8	744	4	US-09-785-381-1	Sequence 1, Appli
20	81	8.8	744	4	US-09-785-381-3	Sequence 3, Appli
21	80.5	8.7	598	2	US-08-853-659A-53	Sequence 53, Appl
22	79	8.5	289	4	US-09-540-236-2019	Sequence 2019, Ap
23	79	8.5	554	4	US-09-252-991A-27968	Sequence 27968, A
24	78.5	8.5	748	3	US-09-061-764A-19	Sequence 19, Appl
25	78	8.4	231	4	US-09-198-452A-419	Sequence 419, App
26	78	8.4	420	4	US-09-134-001C-3805	Sequence 3805, Ap
27	78	8.4	424	4	US-09-543-681A-7510	Sequence 7510, Ap
28	78	8.4	970	4	US-09-795-927-7	Sequence 7, Appli
29	78	8.4	1053	4	US-09-328-352-5058	Sequence 5058, Ap
30	77.5	8.4	492	4	US-09-134-000C-4808	Sequence 4808, Ap
31	77	8.3	154	1	US-08-366-783-5	Sequence 5, Appli
32	77	8.3	292	4	US-09-489-039A-12212	Sequence 12212, A
33	77	8.3	720	4	US-09-134-000C-5631	Sequence 5631, Ap
34	76.5	8.3	601	4	US-09-134-000C-5783	Sequence 5783, Ap
35	76	8.2	700	4	US-09-543-681A-4969	Sequence 4969, Ap
36	76	8.2	993	4	US-08-836-687B-30	Sequence 30, Appl
37	75.5	8.2	231	4	US-09-724-623-116	Sequence 116, App
38	75.5	8.2	408	4	US-09-107-532A-6198	Sequence 6198, Ap
39	75.5	8.2	444	4	US-09-543-681A-5355	Sequence 5355, Ap
40	75.5	8.2	454	4	US-09-904-615-165	Sequence 165, App
41	75.5	8.2	501	4	US-09-328-352-5227	Sequence 5227, Ap
42	75.5	8.2	613	4	US-09-107-532A-6935	Sequence 6935, Ap
43	75	8.1	871	4	US-09-255-829-2	Sequence 2, Appli
44	75	8.1	871	4	US-09-255-829-8	Sequence 8, Appli
45	75	8.1	871	4	US-09-255-829-26	Sequence 26, Appl

ALIGNMENTS

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RESULT 1
US-08-700-607-1
; Sequence 1, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
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;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/700,607
;       FILING DATE:  Filed Herewith
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0114 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  199 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     IMMEDIATE SOURCE:
;       LIBRARY:
;       CLONE:  Consensus
US-08-700-607-1

  Query Match             97.7%;  Score 904;  DB 2;  Length 199;
  Best Local Similarity   97.3%;  Pred. No. 5.7e-89;
  Matches  183;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
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Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
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Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAD 189
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Db        192 PGLKRKAE 199


RESULT 2
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
```

```
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,607
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0114 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  208 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  307311
US-08-700-607-7

  Query Match             73.4%;  Score 679;  DB 2;  Length 208;
  Best Local Similarity   67.9%;  Pred. No. 7.5e-65;
  Matches  127;  Conservative   31;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
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Db         22 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 81

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Db         82 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 141

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|| ||| ||||    :   :||||||||
Db        142 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 201

Qy        183 GLKRKAD 189
              | || |:
Db        202 GAKRHAE 208
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RESULT 3
US-08-700-607-6
; Sequence 6, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307309
US-08-700-607-6

Query Match 73.4%; Score 679; DB 2; Length 356;
Best Local Similarity 67.9%; Pred. No. 1.6e-64;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

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              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        170 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 229

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :||||:|||||||| ||||||||||||
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Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
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Db        290 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 349

Qy        183 GLKRKAD 189
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Db        350 GAKRHAE 356


RESULT 4
US-08-700-607-5
; Sequence 5, Application US/08700607
; Patent No. 5858708
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Hillman, Jennifer L.
;    TITLE OF INVENTION:  TWO NOVEL HUMAN NSP-LIKE PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,607
;      FILING DATE:  Filed Herewith
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0114 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  776 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  307307
US-08-700-607-5

  Query Match             73.4%;  Score 679;  DB 2;  Length 776;
  Best Local Similarity   67.9%;  Pred. No. 4.6e-64;
  Matches  127;  Conservative   31;  Mismatches   29;  Indels    0;  Gaps    0;
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Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        590 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 649

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
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Db        650 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 709

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
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Db        710 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 769

Qy        183 GLKRKAD 189
              | || |:
Db        770 GAKRHAE 776
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RESULT 5
US-08-700-607-8
; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  281046
US-08-700-607-8

  Query Match             71.9%;  Score 665;  DB 2;  Length 267;
  Best Local Similarity   67.2%;  Pred. No. 3.3e-63;
  Matches  123;  Conservative   32;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db         13 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :||||:|||||||| ||||||||||
Db         73 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFAVLM 132

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RESULT 6
US-09-149-476-563
; Sequence 563, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
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;  EARLIER APPLICATION NUMBER: 60/047,615
;  EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060

; EARLIER FILING DATE: 1997-10-02

  Query Match 58.3%; Score 539.5; DB 4; Length 168;
  Best Local Similarity 59.3%; Pred. No. 4.8e-50;
  Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;

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Qy         24 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEE 83
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Db          1 MLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy         84 LVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALI 143
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Db         61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAEL 120

Qy        144 SLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGL-KRKAD 189
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Db        121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 167
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RESULT 7
US-08-700-607-3
; Sequence 3, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
;   APPLICANT: Bandman, Olga
;   APPLICANT: Au-Young, Janice
;   APPLICANT: Goli, Surya K.
;   APPLICANT: Hillman, Jennifer L.
;   TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
;   NUMBER OF SEQUENCES: 9
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Incyte Pharmaceuticals, Inc.
;   STREET: 3174 Porter Drive
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: U.S.
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/700,607
;   FILING DATE: Filed Herewith
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0114 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 241 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    IMMEDIATE SOURCE:
;      LIBRARY:  THP1NOB01
;      CLONE:  31870
US-08-700-607-3

  Query Match             55.8%;  Score 516;  DB 2;  Length 241;
  Best Local Similarity   59.9%;  Pred. No. 2.6e-47;
  Matches   94;  Conservative   33;  Mismatches   30;  Indels    0;  Gaps    0;

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Db         47 AVHDLIXWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA 106

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
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Db        107 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 166

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 157
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Db        167 FMWLMTYVGAVFNGITLLILAELLIXSVPIVYXKYKV 203


RESULT 8
US-09-149-476-411
; Sequence 411, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 186 Human Secreted proteins
;  FILE REFERENCE: PZ002P1
;  CURRENT APPLICATION NUMBER: US/09/149,476
;  CURRENT FILING DATE: 1998-09-08
;  EARLIER APPLICATION NUMBER: PCT/US98/04493
;  EARLIER FILING DATE: 1998-03-06
;  EARLIER APPLICATION NUMBER: 60/040,162
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/040,333
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 30.9%; Score 286; DB 4; Length 92;

```
  Best Local Similarity   56.0%;  Pred. No. 2.9e-23;
  Matches   51;  Conservative   21;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         90 NSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIP 149
              |:|: |:|  :| : |||||:||||||| || ||: |||||:|||:|||||| : :||:|
Db          2 NAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAELLIFSVP 61

Qy        150 VIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ::||::: |||||:|:|    |  : || :|
Db         62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92


RESULT 9
US-08-905-223-411
; Sequence 411, Application US/08905223
; Patent No. 6222029
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Jean-Baptiste D.
;    APPLICANT:  Duelert, Aymeric
;    APPLICANT:  Lacroix, Bruno
;    TITLE OF INVENTION:  5' ESTs FOR SECRETED PROTEINS
;    NUMBER OF SEQUENCES:  503
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  501 West Broadway
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-3505
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Win95
;      SOFTWARE:  Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,223
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  411:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  80 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      TISSUE TYPE:  Brain
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  -78..-1
```

```
;       IDENTIFICATION METHOD:  Von Heijne matrix
;       OTHER INFORMATION:  score 6.3
;       OTHER INFORMATION:  seq TLIMLLSWQLSVS/SV
US-08-905-223-411

  Query Match             10.8%;  Score 100;  DB 3;  Length 80;
  Best Local Similarity   57.1%;  Pred. No. 0.002;
  Matches   20;  Conservative    8;  Mismatches    5;  Indels    2;  Gaps    1;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLS--LTVFSI 33
              :| ||::|||:|||| ||| :| :|||  |:| |:
Db         46 AVHDLIFWRDVKKTGFVFGTTLIMLLSWQLSVSSV 80


RESULT 10
US-08-487-596-8
; Sequence 8, Application US/08487596
; Patent No. 6440681
;  GENERAL INFORMATION:
;    APPLICANT:  Elliot, Kathryn J.
;    APPLICANT:  Ellis, Steven B.
;    APPLICANT:  Harpold, Michael M.
;    TITLE OF INVENTION:  METHODS FOR IDENTIFYING AGONISTS AND
;    TITLE OF INVENTION:  ANTAGONISTS FOR HUMAN NEURONAL
;    TITLE OF INVENTION:  NICOTINIC ACETYLCHOLINE RECEPTORS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,596
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO US94/02447
;      FILING DATE:  08-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/149,503
;      FILING DATE:  08-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/028,031
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/938,154
;      FILING DATE:  30-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/504,455
;      FILING DATE:  03-APR-1990
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-9951
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-238-0999
;      TELEFAX:  619-238-0062
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-487-596-8

  Query Match             10.3%;  Score 95;  DB 4;  Length 468;
  Best Local Similarity   21.5%;  Pred. No. 0.078;
  Matches   41;  Conservative   33;  Mismatches   61;  Indels   56;  Gaps    7;

Qy         24 LLLSLTVFSIV----------SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP- 69
              :|:||||| :|              :  |:   :: ||:|  :    |    :|   |
Db        288 VLVSLTVFLLVIEEIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHHRSSSTHNA 347

Qy         70 ------------------FRAYLESEVAISEELVQ----KYSNSALGHVNSTIKELRRLF 107
                               |::::      ||       | | : |    ::|: : |
Db        348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy        108 L----VDDLVDSLKF------AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 157
              :    | ::|:  ||       : :| | :|          |:  : || :||||:   :
Db        408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS---------IVGSLGLF-VPVIYKWANI 457

Qy        158 QIDHYLGLANK 168
               |  ::| |||
Db        458 LIPVHIGNANK 468


RESULT 11
US-08-660-451A-8
; Sequence 8, Application US/08660451A
; Patent No. 6524789
;  GENERAL INFORMATION:
;    APPLICANT:  Elliott, Kathryn J.
;    APPLICANT:  Harpold, Michael M.
;    TITLE OF INVENTION:  HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
;    TITLE OF INVENTION:  RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
```

```
;       SOFTWARE:  FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/660,451A
;       FILING DATE:  June 7, 1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/484,722
;       FILING DATE:  06/07/95
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Seidman, Stephanie L
;       REGISTRATION NUMBER:  33,779
;       REFERENCE/DOCKET NUMBER:  6362-9370B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-238-0999
;       TELEFAX:  619-238-0062
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  468 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  N-terminal
;     ORIGINAL SOURCE:
US-08-660-451A-8

  Query Match             10.3%;  Score 95;  DB 4;  Length 468;
  Best Local Similarity   21.5%;  Pred. No. 0.078;
  Matches   41;  Conservative   33;  Mismatches   61;  Indels   56;  Gaps    7;

Qy         24 LLLSLTVFSIV----------SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP- 69
              :|:||||| :|              :  |:   :: ||:|  :    |    :|   |
Db        288 VLVSLTVFLLVIEEIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHHRSSSTHNA 347

Qy         70 ------------------FRAYLESEVAISEELVQ----KYSNSALGHVNSTIKELRRLF 107
                               |::::      ||       | | : |    ::|: : |
Db        348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHI 407

Qy        108 L----VDDLVDSLKF------AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 157
              :    | ::|:  ||       : :| | :|          |:  : || :||||:   :
Db        408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS---------IVGSLGLF-VPVIYKWANI 457

Qy        158 QIDHYLGLANK 168
               |  ::| |||
Db        458 LIPVHIGNANK 468


RESULT 12
US-09-462-136-2
; Sequence 2, Application US/09462136
; Patent No. 6426198
; GENERAL INFORMATION:
;  APPLICANT:  Carstea, et al.
;  TITLE OF INVENTION:  Genes for Niemann-Pick Type C Disease
```

```
;  FILE REFERENCE:  4239-53894
;  CURRENT APPLICATION NUMBER: US/09/462,136
;  CURRENT FILING DATE:  2000-06-01
;  PRIOR APPLICATION NUMBER:  PCT/US98/13862
;  PRIOR FILING DATE:  1998-07-02
;  PRIOR APPLICATION NUMBER:  US 60/051,682
;  PRIOR FILING DATE:  1997-07-03
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1278
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-462-136-2

  Query Match              9.6%;  Score 88.5;  DB 4;  Length 1278;
  Best Local Similarity   25.7%;  Pred. No. 1.6;
  Matches   39;  Conservative   25;  Mismatches   51;  Indels   37;  Gaps    7;

Qy         46 SVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 105
              ::||||   : :   : :  :   |       | ||  ::  | : ||||    ||  ||
Db        598 NLTISFTAERSIEDELNRESDSDVF------TVVISYAIMFLYISLALGH----IKSCRR 647

Qy        106 LFLVDD---------LVDSLKFAVLMWVFTYVGALFNGLTLLILALI----------SLF 146
              | |||          |:     |  : ||:|:|     |||::: :|          ::|
Db        648 L-LVDSKVSLGIAGILIVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703

Qy        147 SIPVIYERHQ----VQIDHYLGLANKSVKDAM 174
               :   |:| :      :|  ||     |  :|
Db        704 ILVQAYQRDERLQGETLDQQLGRVLGEVAPSM 735


RESULT 13
US-09-134-000C-5477
; Sequence 5477, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5477
;   LENGTH: 592
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-5477

  Query Match              9.4%;  Score 86.5;  DB 4;  Length 592;
  Best Local Similarity   20.9%;  Pred. No. 0.88;
  Matches   49;  Conservative   41;  Mismatches   61;  Indels   83;  Gaps   12;
```

```
Qy          7 YWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR----------IYK 55
              :|: :|:        ||  :|  : ||::|   : ||: :|    :           |:|
Db         45 FWKTVKR--------LFRYMSKRMLSIIAV---LVLAIAAVVFQIQTPKVLGQATTEIFK 93

Qy         56 GVIQAIQKSDEGHPFRA-----------------YLESEV-----------------A 79
              ||::   :  :|    :                  || | |
Db         94 GVMKGAAEMKQGLKITSFPIDFDKIGQILLIVIAMYLISAVFNFLQQVIMTRVSQRTVYE 153

Qy         80 ISEELVQKYSNSALG----HVNSTIKELRRLFLVDDLVDSLK---FAVLMWVFTYVGALF 132
              : :||  | :   :     | |  |   | :  :|::  :|:     ::  : |:|| |:
Db        154 LRQELEAKMNKVPISYYDIHSNGDIMS-RAINDMDNIASTLQQNLTQLITSIVTFVGVLW 212

Qy        133 NGLT----LLILAL----ISLFSIPVIYERHQVQIDHY------LGLANKSVKD 172
                ||    | ::||    :||  : |:  | |    |:      ||| |  |::
Db        213 MMLTISWQLTLIALATVPLSLIVVMVVAPRSQ---KHFAAQQKSLGLLNNQVEE 263


RESULT 14
US-08-956-171E-5246
; Sequence 5246, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
```

```
;              TELEFAX: (301) 309-8439
;    INFORMATION FOR SEQ ID NO: 5246:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 414 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 5246:
US-08-956-171E-5246

  Query Match              9.3%;  Score 86;  DB 4;  Length 414;
  Best Local Similarity   22.2%;  Pred. No. 0.61;
  Matches   42;  Conservative   37;  Mismatches   78;  Indels   32;  Gaps    7;

Qy          2 VVDLLYWRDIKKTGV-VFGASLFLLLSLTVFSIVSVTAYI-ALALLSVTISFRIYKGVIQ 59
              :| ||: |:|: | : :    | ||::|    :  |:  |  |  |:| |  |:    |
Db          3 IVILLFLRNIRTTAISIISIPLSLLMALIALKLSDVSLNILTLGALTVAIG-RVIDDSIV 61

Qy         60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 119
               ::     : :|   :||  :  | :          : |   |: :  :   ||  : |
Db         62 VVE-----NIYRRLTDSEEQLKGENL----------IISATTEVFKPIMSSTLVTIIVFL 106

Qy        120 VLMWVFTYVGALFN------GLTLLILALISLFSIPVI--------YERHQVQIDHYLGL 165
               |::|   || :|         :||   |:|:  :| :          :|   |    ||:
Db        107 PLVFVSGSVGEMFRPFALAIAFSLLASLLVSITLVPALAATLFKKGVKRRNKQHQEGLGV 166

Qy        166 ANKSVKDAM 174
               : : |  :
Db        167 VSTTYKKVL 175


RESULT 15
US-09-134-001C-5005
; Sequence 5005, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5005
;   LENGTH: 1051
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5005

  Query Match              9.2%;  Score 85.5;  DB 4;  Length 1051;
  Best Local Similarity   22.1%;  Pred. No. 2.5;
```

```
  Matches   43;  Conservative   39;  Mismatches   62;  Indels   51;  Gaps    9;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSV-----TAYIALALLSVTISFRIYKG 56
              :| ||: |:|: | :               ||||:      | ||| | :|:::
Db        380 IVILLFLRNIRTTAI---------------SIVSIPMSILIALIALKLSNVSLNILTLGA 424

Qy         57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYS--NSALGHVNSTIKELRRLF---LVDD 111
              :  || :          ::  : : | : :: |  |  |   |  |   | :|   :
Db        425 LTVAIGR---------VIDDSIVVVENIFRRLSDPNEKLKGENLIISATREVFKPIMSST 475

Qy        112 LVDSLKFAVLMWVFTYVGALFN----GLTLLILA--LISLFSIPVI---YERHQVQIDHY 162
              ||  : |  |::|   || :|      :|  :||  |:|:  :| :   : ::
Db        476 LVTIVVFLPLVFVSGSVGEMFRPFALAITFSLLASLLVSITLVPSLGATFFKN------- 528

Qy        163 LGLANKSVKDAMAKI 177
               |: |:  |: :  :
Db        529 -GVKNREQKEGLGTV 542


Search completed: September 29, 2004, 18:21:00
Job time : 6.69196 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:05:43 ; Search time 4.62587 Seconds
(without alignments)
3930.111 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	679	73.4	208	2	I60904	neuroendocrine-spe
2	679	73.4	776	2	A46583	neuroendocrine-spe
3	665	71.9	267	2	A60021	tropomyosin-relate
4	321	34.7	2484	2	T26216	hypothetical prote
5	321	34.7	2607	2	T26215	hypothetical prote
6	320	34.6	222	2	T26213	hypothetical prote
7	194	21.0	255	2	E84899	hypothetical prote
8	182	19.7	271	2	T13013	hypothetical prote
9	163	17.6	275	2	T05595	hypothetical prote
10	142	15.4	393	2	S67763	probable membrane
11	135.5	14.6	242	2	B85016	hypothetical prote
12	134	14.5	183	2	A84527	hypothetical prote
13	131.5	14.2	295	2	S59439	probable membrane

14	123	13.3	206	2	T01153	probable seed matu
15	109.5	11.8	264	2	T47948	hypothetical prote
16	107.5	11.6	203	2	T47571	hypothetical prote
17	94	10.2	288	2	B90043	conserved hypothet
18	93.5	10.1	457	2	H85095	hypothetical prote
19	92.5	10.0	458	2	A72258	hypothetical prote
20	92.5	10.0	677	2	F95232	immunity protein,
21	92.5	10.0	680	2	H98096	conserved hypothet
22	91	9.8	160	2	C84422	hypothetical prote
23	90.5	9.8	442	2	C75057	hypothetical prote
24	89	9.6	224	2	D71915	hydrogenase, cytoc
25	89	9.6	468	2	A38223	nicotinic acetylch
26	87	9.4	1065	2	E69795	acriflavin resista
27	86	9.3	589	2	F64201	transport ATP-bind
28	86	9.3	1055	2	H90023	hypothetical prote
29	85.5	9.2	296	2	S46018	probable membrane
30	85.5	9.2	299	2	B69155	hypothetical prote
31	85	9.2	299	2	C64397	hypothetical prote
32	85	9.2	459	2	G86264	F3F19 hypothetical
33	85	9.2	689	2	T09007	ABC-transporter ho
34	84.5	9.1	151	2	G96705	unknown protein, 7
35	83.5	9.0	445	2	AD2358	glucosyltransferas
36	83.5	9.0	570	2	S52765	secD protein - Str
37	83.5	9.0	823	2	H83724	hypothetical prote
38	83	9.0	180	2	E97200	probable phosphata
39	83	9.0	252	2	G97886	hypothetical prote
40	83	9.0	388	1	D70006	conserved hypothet
41	82.5	8.9	410	2	A95044	conserved hypothet
42	82.5	8.9	502	2	F70316	conserved hypothet
43	82.5	8.9	675	2	T50332	SCT1 homolog SPBC1
44	82.5	8.9	937	2	T41400	probable peroxisom
45	82	8.9	224	1	A64599	hydrogenase (EC 1.

ALIGNMENTS

RESULT 1
I60904
neuroendocrine-specific protein C - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: I60904
R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.
J. Biol. Chem. 268, 13439-13447, 1993
A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.
A;Reference number: A46583; MUID:93293865; PMID:7685762
A;Accession: I60904
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-208 <RES>
A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311
C;Genetics:
A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 73.4%; Score 679; DB 2; Length 208;
Best Local Similarity 67.9%; Pred. No. 2.5e-52;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

```
Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db         22 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 81

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :||||:|||||||| ||||||||||||
Db         82 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 141

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|| ||| |||    :   :||||||||
Db        142 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 201

Qy        183 GLKRKAD 189
              | || |:
Db        202 GAKRHAE 208
```

RESULT 2
A46583
neuroendocrine-specific protein, splice form A - human
N;Contains: neuroendocrine-specific protein, splice form B
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: A46583; I60903
R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.
J. Biol. Chem. 268, 13439-13447, 1993
A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.
A;Reference number: A46583; MUID:93293865; PMID:7685762
A;Accession: A46583
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-776 <ROE1>
A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307
A;Accession: I60903
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 421-776 <ROE2>
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
C;Genetics:
A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 73.4%; Score 679; DB 2; Length 776;
Best Local Similarity 67.9%; Pred. No. 1.2e-51;
Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

```
Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        590 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 649

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :||||:|||||||| ||||||||||
Db        650 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 709

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|| ||| |||| :  :|||||||
Db        710 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 769

Qy        183 GLKRKAD 189
              | || |:
Db        770 GAKRHAE 776


RESULT 3
A60021
tropomyosin-related protein, neuronal - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Nov-1999
C;Accession: A60021
R;Wieczorek, D.F.; Hughes, S.R.
Brain Res. Mol. Brain Res. 10, 33-41, 1991
A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.
A;Reference number: A60021; MUID:91278684; PMID:1647480
A;Accession: A60021
A;Molecule type: mRNA
A;Residues: 1-267 <WIE>
A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550
C;Comment: This neuronal-specific mRNA was identified by hybridization to an
alpha-tropomyosin probe but does not show homology in amino acid sequence.

  Query Match             71.9%;  Score 665;  DB 2;  Length 267;
  Best Local Similarity   67.2%;  Pred. No. 5.7e-51;
  Matches  123;  Conservative   32;  Mismatches   28;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db         13 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :||||:|||||||| ||||||||||
Db         73 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFAVLM 132

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|| |:| |||| :  :|||||||
Db        133 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQAKIP 192

Qy        183 GLK 185
              | :
Db        193 GAR 195


RESULT 4
T26216
```

hypothetical protein W06A7.3c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26216
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26216
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2484 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3c
A;Map position: 5
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

  Query Match 34.7%; Score 321; DB 2; Length 2484;
  Best Local Similarity 32.6%; Pred. No. 1.1e-19;
  Matches 60; Conservative 46; Mismatches 78; Indels 0; Gaps 0;

```
Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:|::|||| ||: :|   :| :|  |  : :::|  |  |  |     ||::| |   |
Db       2289 VLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFRVFKKVEAQI 2348

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              :|:|  |||   |  :: : :| |   ::  : |      :|::|  |:  ::|:|| ::
Db       2349 KKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFGLV 2408

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              :|  ||: : |:| || || |: :||:| :|| :|  || :|   :  :|:    |  |:
Db       2409 LWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL 2468

Qy        182 PGLK 185
              | |:
Db       2469 PFLR 2472
```

RESULT 5
T26215
hypothetical protein W06A7.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26215
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26215
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2607 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3a
A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
2586/2

Query Match 34.7%; Score 321; DB 2; Length 2607;
Best Local Similarity 32.6%; Pred. No. 1.2e-19;
Matches 60; Conservative 46; Mismatches 78; Indels 0; Gaps 0;

```
Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:|::|||| ||: :|   :| :|  |  : :::|  |  |  |     ||::| |   |
Db       2412 VLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFRVFKKVEAQI 2471

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              :|:|  |||   |  :: : :| |   ::  : |      :|::|  |:  ::|:|| ::
Db       2472 KKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFGLV 2531

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              :|  ||: : |:| || || |: :||:| :|| :|  || :|   :  :|:    |  |:
Db       2532 LWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL 2591

Qy        182 PGLK 185
              | |:
Db       2592 PFLR 2595
```

RESULT 6
T26213
hypothetical protein W06A7.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26213
R;Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z20173
A;Accession: T26213
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-222 <WIL>
A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b
A;Experimental source: clone W06A7
C;Genetics:
A;Gene: CESP:W06A7.3b
A;Map position: 5
A;Introns: 27/1; 77/2; 201/2

Query Match 34.6%; Score 320; DB 2; Length 222;
Best Local Similarity 32.1%; Pred. No. 8.5e-21;
Matches 59; Conservative 47; Mismatches 78; Indels 0; Gaps 0;

```
Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ::|::|||| ||: :|   :| :|  |  : :::|  |  |  |     ||::| |   |
Db         27 ILDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTYSLLLALGAAAGFRVFKKVEAQI 86

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              :|:|  |||   |  :: : :| |   ::  : |      :|::|  |:  ::|:|| ::
Db         87 KKTDSEHPFSEILAQDLTLPQEKVHAQADVFVEHATCIANKLKKLVFVESPLESIKFGLV 146

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
```

```
            :|  ||: : |:| || || |: :||:| :|| :|  || :|   :  :|:    |  |:
Db        147 LWSLTYIASWFSGFTLAILGLLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKL 206

Qy        182 PGLK 185
              | |:
Db        207 PFLR 210
```

RESULT 7
E84899
hypothetical protein At2g46170 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84899
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84899
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-255 <STO>
A;Cross-references: GB:AE002093; NID:g3702332; PIDN:AAC62889.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g46170
A;Map position: 2

Query Match 21.0%; Score 194; DB 2; Length 255;
Best Local Similarity 27.6%; Pred. No. 1.1e-09;
Matches 54; Conservative 41; Mismatches 77; Indels 24; Gaps 6;

```
Qy          4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:  ||| | :| | |   ::::|  |  : ::|:  :|::  |       ::      |
Db         70 DVFLWRDKKLSGAVLGVATAIWVLFELVEYHLLSLLCHISILALG---GLFLWSNAHTLI 126

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
               |:    |       |: : ||     ::|    :|     || : |  ||   |   |
Db        127 NKTSPQIP-------EIHVPEEAFLVVASSLRNELNQAFVILRSIALGRDLKKFLMVVVG 179

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM------- 174
              :|: : ||  || |||: :  : | ::|::||:|: ::|    || |::|:
Db        180 LWIISVVGNWFNFLTLVYICFVILHTVPMLYEKHEDKVD---PLAEKAMKELQKQYVVFD 236

Qy        175 AKIQAKIP--GLKRKA 188
               |: :|||   || ||
Db        237 EKVLSKIPIASLKAKA 252
```

RESULT 8
T13013

hypothetical protein F8L21.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 22-Oct-1999
C;Accession: T13013
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.
submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17587
A;Accession: T13013
A;Molecule type: DNA
A;Residues: 1-271 <BEV>
A;Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.10
A;Experimental source: cultivar Columbia; BAC clone F8L21
C;Genetics:
A;Gene: ATSP:F8L21.10
A;Map position: 4
A;Introns: 85/1; 145/2; 192/3; 216/1

Query Match 19.7%; Score 182; DB 2; Length 271;
Best Local Similarity 25.6%; Pred. No. 1.4e-08;
Matches 46; Conservative 43; Mismatches 79; Indels 12; Gaps 3;

```
Qy          4 DLLYWRDIKKTGVVFGAS--LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:  |:| | :| |||  :   ::|  |  : ::::  :: :  |:|     ::      |
Db         87 DIFMWKDKKMSGGVFGGATVAWVLFELMEYHLLTLLCHVMIVALAVLF---LWSNATMFI 143

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
               ||    |       || | || : : ::     :|  |  || :    |:   |
Db        144 HKSPPKIP-------EVHIPEEPLLQLASGLRIEINRGISSLREIASGRDIKKFLSAIAG 196

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              :|| : :|  :: |||  :||: ||::|: |:::: ::| |   |   :|   | : ||:
Db        197 LWVLSILGGCYSFLTLAYIALVLLFTVPLFYDKYEDKVDSYGEKAMAELKKQYAVLDAKV 256
```

RESULT 9
T05595
hypothetical protein F9D16.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C;Accession: T05595
R;Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15419
A;Accession: T05595
A;Molecule type: DNA
A;Residues: 1-275 <BEV>
A;Cross-references: EMBL:AL035394
A;Experimental source: cultivar Columbia; BAC clone F9D16
C;Genetics:
A;Map position: 4
A;Introns: 89/1; 149/2; 196/3; 220/1
A;Note: F9D16.100

Query Match 17.6%; Score 163; DB 2; Length 275;
Best Local Similarity 25.5%; Pred. No. 6.4e-07;

```
  Matches   49;  Conservative   43;  Mismatches   82;  Indels   18;  Gaps    5;

Qy          4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |:  |:: | :| | |   : :::  |  : ::::  :: : :|:|     ::      |
Db         91 DIFMWKNKKMSGGVLGGATAAWVVFELMEYHLLTLLCHVMIVVLAVLF---LWSNATMFI 147

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
               ||    |       || | || : : ::     :|     || :    ||   |
Db        148 NKSPPKIP-------EVHIPEEPILQLASGLRIEINRGFSSLREIASGRDLKKFLIAIAG 200

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMA----KI 177
              :|| : :|  || |||  :||: ||::|: |:::: ::|     |   :|   |    |:
Db        201 LWVLSILGGCFNFLTLAYIALVLLFTVPLAYDKYEDKVDPLGEKAMIELKKQYAVLDEKV 260

Qy        178 QAKIP--GLKRK 187
              :|||   || |
Db        261 LSKIPLGPLKNK 272


RESULT 10
S67763
probable membrane protein YDL204w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein D1062
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67763
R;Schmidt, E.R.; Bahr, A.; Kraemer, C.; Hankeln, T.; Moeller-Rieker, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67756
A;Accession: S67763
A;Molecule type: DNA
A;Residues: 1-393 <SCH>
A;Cross-references: EMBL:Z74252; NID:g1431337; PID:e253109; PID:g1431338;
GSPDB:GN00004; MIPS:YDL204w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YDL204w
A;Cross-references: SGD:S0002363
A;Map position: 4L
C;Keywords: transmembrane protein
F;50-66/Domain: transmembrane #status predicted <TM1>
F;150-166/Domain: transmembrane #status predicted <TM2>

  Query Match             15.4%;  Score 142;  DB 2;  Length 393;
  Best Local Similarity   26.3%;  Pred. No. 6.8e-05;
  Matches   45;  Conservative   34;  Mismatches   56;  Indels   36;  Gaps    4;

Qy          5 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKS 64
              |:|| :  |:|  | |:|  || |   :::||   |   :|  :
Db         33 LIYWTNPSKSGASFAATLVSLLILRNVNVISVLLKIGYMVLFTS---------------- 76

Qy         65 DEGHPFRAYLESEVAISEELVQKY----SNSALGHVNSTI-KELRRLFLVDDLVDSLKFA 119
                   |   | ::|   : :| ::    |   :| :   | :|| ||  ::| :  | ||
Db         77 -----FAVELSTKVLFDKGVVSRFGMQESPDLVGVLKPHIDRELDRLPALEDRIRKLVFA 131

Qy        120 ----------VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQID 160
                       | ::    : |:|:  |:||:  | |:::|:||:| | :||
```

```
Db        132 HRTRNNFTIGVSLYFLHGLFAIFSMNTVLIMTTIFLYTVPLIYDRKQARID 182


RESULT 11
B85016
hypothetical protein AT4g01230 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: B85016
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The
Cold Spring Harbor, Washington University in St Louis and PE Biosystems
Arabidopsis Sequencing Consortium.
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85016
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <STO>
A;Cross-references: GB:NC_001268; NID:g7267620; PIDN:CAB80932.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4g01230
A;Map position: 4

  Query Match             14.6%;  Score 135.5;  DB 2;  Length 242;
  Best Local Similarity   23.8%;  Pred. No. 0.00014;
  Matches   46;  Conservative   49;  Mismatches   63;  Indels   35;  Gaps    7;

Qy          4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIV-------SVTAYIALALLSVTISFRIYKG 56
              |:| ||| | |       | || ::||  ::        :|:    ::| : :|| ::
Db         70 DVLLWRDKKVT-------LGLLSAVTVIWLLFGFGGRRLLTSLCRGSILFLLLSF-LWS- 120

Qy         57 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSL 116
                 |: || |          :: | |: : : :::    :|     || : |  |: : :
Db        121 --NALNKSPEN-------MMDIYIPEKPLLQAASAMTFELNCAFATLRSIALERDIKNFV 171

Qy        117 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAM-- 174
                : :|: : :|  |: |:|| :  : : ::|::||::: :||    :| |:| :
Db        172 MAVIGLWLVSVIGNWFSFLSLLYICFVLIHTVPMLYEKYEDEID---PIAEKAVIEMKKH 228

Qy        175 -----AKIQAKIP 182
                    ||  :|||
Db        229 YQVFEAKFLSKIP 241


RESULT 12
A84527
hypothetical protein At2g15280 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84527
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,
C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,
L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,
M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,
```

G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84527
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <STO>
A;Cross-references: GB:AE002093; NID:g4662633; PIDN:AAD26905.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g15280
A;Map position: 2

Query Match 14.5%; Score 134; DB 2; Length 183;
Best Local Similarity 24.6%; Pred. No. 0.00014;
Matches 44; Conservative 38; Mismatches 79; Indels 18; Gaps 4;

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Qy          8 WRDIKKTGVVFGAS-----LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              |:: :   :: |::     ||     : |  |     :   |||| | |   |  |
Db          2 WKNRRGGFLLLGSTTLLWFLFEKCGYSFFPFV-----VNTQLLSVVILFLWAKSAI---- 52

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
               :   |    ||    |:|| |   :::    :|: :   | :::  :     : :|::
Db         53 LFNRPMPQLPNLE----ITEEFVFMVADAIRVWINTVLAVAREIYVGRNAKQLFRVSVVL 108

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              |  ::||   | ||:| | ::    || :|||:|  ||  | | :: ::    ||  ::
Db        109 WTVSFVGNFLNFLTILYLGVVLSLLIPFLYERYQDLIDEKLSLTHRVIQTQYRKIDERL 167
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RESULT 13
S59439
probable membrane protein YDR233c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YD9934.17c
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59439
R;Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S59423
A;Accession: S59439
A;Molecule type: DNA
A;Residues: 1-295 <MUR>
A;Cross-references: EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004; MIPS:YDR233c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YDR233c
A;Cross-references: SGD:S0002641
A;Map position: 4R
C;Keywords: transmembrane protein
F;40-56/Domain: transmembrane #status predicted <TM1>
F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 14.2%; Score 131.5; DB 2; Length 295;

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  Best Local Similarity   21.6%;  Pred. No. 0.0004;
  Matches   45;  Conservative   43;  Mismatches   69;  Indels   51;  Gaps    5;

Qy          4 DLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQK 63
              ||| ||:  :||  || ||  || |   ::::    :|  :|  |       | |: :
Db         22 DLLLWRNPVQTGKYFGGSLLALLILKKVNLITFFLKVAYTILFTT-------GSIEFV-- 72

Qy         64 SDEGHPFRAYLESEVAISEELVQKY--------SNSALGHVNSTIKEL-------RRLFL 108
                        |:: : : |: ||        :     |::  :|:|       |:
Db         73 ------------SKLFLGQGLITKYGPKECPNIAGFIKPHIDEALKQLPVFQAHIRKTVF 120

Qy        109 VDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQID-------- 160
                 : | || :::     : |:  |:: :| |  |::|||  :: :||
Db        121 AQVPKHTFKTAVALFLLHKFFSWFSIWTIVFVADIFTFTLPVIYHSYKHEIDATVAQGVE 180

Qy        161 -------HYLGLANKSVKDAMAKIQAKI 181
                    :  :| :  |  : |:::|:
Db        181 ISKQKTQEFSQMACEKTKPYLDKVESKL 208
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RESULT 14
T01153
probable seed maturation protein [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F27L4.17
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T01153; T02426; C84627
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
A;Reference number: Z14198
A;Accession: T01153
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <ROU>
A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242725
A;Experimental source: cultivar Columbia
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C.
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence.
A;Reference number: Z14658
A;Accession: T02426
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-206 <RO2>
A;Cross-references: EMBL:AC004482; NID:g3152602; PIDN:AAC17096.1; PID:g3152617
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84627
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <STO>
A;Cross-references: GB:AE002093; NID:g3152617; PIDN:AAC17096.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g23640; F26B6.29; F27L4.17
A;Map position: 2
A;Introns: 14/1; 76/2; 147/1
C;Superfamily: Arabidopsis thaliana hypothetical protein F27L4.17

Query Match 13.3%; Score 123; DB 2; Length 206;
Best Local Similarity 20.9%; Pred. No. 0.0015;
Matches 40; Conservative 48; Mismatches 85; Indels 18; Gaps 4;

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Qy          2 VVDLLYWRDIKK--TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 59
              | |:  ||  |   : ::   | ::|||   |: ::: ::| :|::|:     ::  :::
Db         16 VEDIYLWRRKKLAFSTLLVSTSTWILLSFYGFTTITIVSWIGIAVVSMIF---LWGSLLR 72

Qy         60 AIQKSDEGHPFRAYLESEVA---ISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSL 116
               : |          :| |::   :||| | :   |    :   :: : |:    :
Db         73 LLSK----------VEPELSGLEVSEEFVVETVRSCRMLMEEMVRWMFRVGAESEWFVFA 122

Qy        117 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAK 176
              :  :  |: : :| | :  | | : |:   ::| ::| :  ||  :||      | |
Db        123 RTVLGFWILSRIGNLLDFHTCLFIGLVMGLTVPKLWEEYGDQIQKHLGSLKDKSKGAYNT 182

Qy        177 IQAKIPGLKRK 187
                ||  :| |
Db        183 THEKILEMKNK 193
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RESULT 15
T47948
hypothetical protein F2A19.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47948
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, M.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480
A;Accession: T47948
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-264 <DEH>
A;Cross-references: EMBL:AL132962
A;Experimental source: cultivar Columbia; BAC clone F2A19
C;Genetics:
A;Map position: 3
A;Introns: 68/1; 128/2; 164/1; 210/1
A;Note: F2A19.160

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  Query Match             11.8%;  Score 109.5;  DB 2;  Length 264;
  Best Local Similarity   24.9%;  Pred. No. 0.03;
  Matches   54;  Conservative   38;  Mismatches   68;  Indels   57;  Gaps   14;

Qy          4 DLLYWRDIKKTGVVFG--ASLFLLLSLTVFSIVSVTAYI------ALALLSVTISFRIYK 55
              |:  ||| | :  | |   ::::|  |  :  :|:  :|      || |||   :| : |
Db         70 DVFLWRDKKLSASVLGVATAIWVLFELVEYHFLSLVCHILIFALAALFLLSNAHAF-MNK 128

Qy         56 GVIQ-----AIQKSDEG------HPFRAYLESEVAISEELVQK-YSN-SALGHVNSTIKE 102
              |          :::: |      |  |  ||    || ||:|  |   | :| |  |
Db        129 GTFPYDCFCTEKRAEPGLCYFKEHCLRKGLEE---ISHELIQSTYETFSIMGFVTRT--- 182

Qy        103 LRRLFLVDDLVDSLKFAVL--MWVFTYVGALFNG--LTLLILALISLFSIPVIYERHQVQ 158
                          |:   :    |    :|    |  : ||    : | ::|::||:|: :
Db        183 ------------SIYIGISGGFWAVDNLGC---GKLVQLLDSCFVVLHTVPMLYEKHEDK 227

Qy        159 IDHYLGLANKSVKDAM-------AKIQAKIPGLKRKA 188
              :|    :| |::|:          |: :|:|    ||
Db        228 VD---PVAEKTLKELKKHYMVFDEKVLSKLPVASLKA 261


Search completed: September 29, 2004, 18:15:52
Job time : 6.62587 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:16:15 ; Search time 20.2878 Seconds
(without alignments)
2997.869 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description

1	925	100.0	1163	9	US-09-893-348-18	Sequence 18, Appl
2	922	99.7	379	14	US-10-205-194-164	Sequence 164, App
3	921	99.6	199	9	US-09-893-348-21	Sequence 21, Appl
4	921	99.6	360	9	US-09-893-348-20	Sequence 20, Appl
5	908	98.2	1192	9	US-09-789-386-2	Sequence 2, Appli
6	908	98.2	1192	9	US-09-758-140-6	Sequence 6, Appli
7	908	98.2	1192	9	US-09-893-348-23	Sequence 23, Appl
8	908	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appli
9	908	98.2	1192	12	US-10-267-502-429	Sequence 429, App
10	908	98.2	1192	14	US-10-060-036-71	Sequence 71, Appl
11	908	98.2	1192	16	US-10-327-213-9	Sequence 9, Appli
12	908	98.2	1192	16	US-10-466-258-9	Sequence 9, Appli
13	906.5	98.0	1163	12	US-10-267-502-431	Sequence 431, App
14	904	97.7	199	9	US-09-893-348-25	Sequence 25, Appl
15	904	97.7	199	12	US-10-660-946-1	Sequence 1, Appli
16	904	97.7	373	9	US-09-789-386-6	Sequence 6, Appli
17	904	97.7	373	9	US-09-765-205-6	Sequence 6, Appli
18	904	97.7	373	9	US-09-893-348-24	Sequence 24, Appl
19	904	97.7	373	12	US-10-408-967-8	Sequence 8, Appli
20	904	97.7	373	14	US-10-060-036-72	Sequence 72, Appl
21	904	97.7	373	16	US-10-466-258-4	Sequence 4, Appli
22	901	97.4	1192	12	US-10-408-967-7	Sequence 7, Appli
23	897	97.0	199	12	US-10-408-967-9	Sequence 9, Appli
24	895	96.8	199	12	US-09-978-360A-467	Sequence 467, App
25	864	93.4	199	16	US-10-466-258-11	Sequence 11, Appl
26	679	73.4	208	12	US-10-660-946-7	Sequence 7, Appli
27	679	73.4	356	12	US-10-660-946-6	Sequence 6, Appli
28	679	73.4	776	12	US-10-660-946-5	Sequence 5, Appli
29	679	73.4	776	12	US-10-267-502-430	Sequence 430, App
30	678	73.3	777	14	US-10-205-219-93	Sequence 93, Appl
31	678	73.3	780	12	US-10-267-502-432	Sequence 432, App
32	665	71.9	267	12	US-10-660-946-8	Sequence 8, Appli
33	665	71.9	267	14	US-10-205-194-127	Sequence 127, App
34	622.5	67.3	236	9	US-09-729-674-20	Sequence 20, Appl
35	622.5	67.3	236	9	US-09-765-205-26	Sequence 26, Appl
36	622.5	67.3	236	12	US-10-408-967-2	Sequence 2, Appli
37	622.5	67.3	266	12	US-10-276-774-2330	Sequence 2330, Ap
38	622.5	67.3	269	14	US-10-106-698-6222	Sequence 6222, Ap
39	617.5	66.8	593	15	US-10-108-260A-2892	Sequence 2892, Ap
40	539.5	58.3	168	10	US-09-809-391-563	Sequence 563, App
41	539.5	58.3	168	10	US-09-882-171-563	Sequence 563, App
42	539.5	58.3	168	12	US-10-164-861-563	Sequence 563, App
43	520	56.2	222	12	US-10-267-502-428	Sequence 428, App
44	516	55.8	241	12	US-10-660-946-3	Sequence 3, Appli
45	507.5	54.9	234	12	US-10-424-599-200840	Sequence 200840,

ALIGNMENTS

RESULT 1
US-09-893-348-18
; Sequence 18, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-18

Query Match 100.0%; Score 925; DB 9; Length 1163;
Best Local Similarity 100.0%; Pred. No. 1e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154

Qy        181 IPGLKRKAD 189
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Db       1155 IPGLKRKAD 1163
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RESULT 2
US-10-205-194-164
; Sequence 164, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

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;  FILE REFERENCE: WL-A-018201
;  CURRENT APPLICATION NUMBER: US/10/205,194
;  CURRENT FILING DATE:  5200-07-24
;  PRIOR APPLICATION NUMBER: GB 0118354.0
;  PRIOR FILING DATE: 2001-07-27
;  NUMBER OF SEQ ID NOS: 177
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
;   LENGTH: 379
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-164

  Query Match             99.7%;  Score 922;  DB 14;  Length 379;
  Best Local Similarity   99.5%;  Pred. No. 4.6e-85;
  Matches  188;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 250

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 310

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 370

Qy        181 IPGLKRKAD 189
              |||||||||
Db        371 IPGLKRKAD 379


RESULT 3
US-09-893-348-21
; Sequence 21, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
```

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;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 199
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-893-348-21

  Query Match             99.6%;  Score 921;  DB 9;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-85;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 191

Qy        182 PGLKRKAD 189
              ||||||||
Db        192 PGLKRKAD 199


RESULT 4
US-09-893-348-20
; Sequence 20, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
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; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20

  Query Match 99.6%; Score 921; DB 9; Length 360;
  Best Local Similarity 100.0%; Pred. No. 5.5e-85;
  Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 232

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 292

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 352

Qy        182 PGLKRKAD 189
              ||||||||
Db        353 PGLKRKAD 360
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RESULT 5
US-09-789-386-2
; Sequence 2, Application US/09789386
; Patent No. US20020010324A1
; GENERAL INFORMATION:
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: PRINJHA, RABINDER KUMAR
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-2

  Query Match 98.2%; Score 908; DB 9; Length 1192;
  Best Local Similarity 97.4%; Pred. No. 5.5e-83;
  Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
              ||||||||:
Db       1184 IPGLKRKAE 1192


RESULT 6
US-09-758-140-6
; Sequence 6, Application US/09758140
; Patent No. US20020012965A1
; GENERAL INFORMATION:
;  APPLICANT:  Strittmatter, Stephen M.
;  TITLE OF INVENTION:  No. US20020012965A1o Receptor-Mediated Blockade of
Axonal Growth
;  FILE REFERENCE:  44574-5073-US
;  CURRENT APPLICATION NUMBER: US/09/758,140
;  CURRENT FILING DATE:  2001-01-12
;  PRIOR APPLICATION NUMBER:  US 60/175,707
;  PRIOR FILING DATE:  2000-01-12
;  PRIOR APPLICATION NUMBER:  US 60/207,366
;  PRIOR FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  US 60/236,378
;  PRIOR FILING DATE:  2000-09-29
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-758-140-6

  Query Match             98.2%;  Score 908;  DB 9;  Length 1192;
  Best Local Similarity   97.4%;  Pred. No. 5.5e-83;
  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
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              ||||||||:
Db       1184 IPGLKRKAE 1192


RESULT 7
US-09-893-348-23
; Sequence 23, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
;  APPLICANT: EISENBACH-SCHWARTZ, Michal
;  APPLICANT:  COHEN, Irun R.
;  APPLICANT:  BESERMAN, Pierre
;  APPLICANT:  MOSONEGO, Alon
;  APPLICANT:  MOALEM, Gila
;  TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
;  FILE REFERENCE: EIS-SCHWARTZ=2A
;  CURRENT APPLICATION NUMBER: US/09/893,348
;  CURRENT FILING DATE:  2001-06-28
;  PRIOR APPLICATION NUMBER: US 09/314,161
;  PRIOR FILING DATE: 1999-05-19
;  PRIOR APPLICATION NUMBER: US 09/218,277
;  PRIOR FILING DATE: 1998-12-22
;  PRIOR APPLICATION NUMBER: PCT/US98/14715
;  PRIOR FILING DATE: 1998-07-21
;  PRIOR APPLICATION NUMBER: IL 124500
;  PRIOR FILING DATE: 1998-05-19
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-893-348-23

  Query Match             98.2%;  Score 908;  DB 9;  Length 1192;
  Best Local Similarity   97.4%;  Pred. No. 5.5e-83;
  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
              ||||||||:
Db       1184 IPGLKRKAE 1192


RESULT 8
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US-09-972-599A-6
; Sequence 6, Application US/09972599A
; Patent No. US20020077295A1
; GENERAL INFORMATION:
; APPLICANT: STRITTMATTER, STEPHEN M.
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH
; FILE REFERENCE: C077 CIP US
; CURRENT APPLICATION NUMBER: US/09/972,599A
; CURRENT FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: PCT/US01/01041
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/758,140
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/236,378
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

Query Match 98.2%; Score 908; DB 9; Length 1192;
Best Local Similarity 97.4%; Pred. No. 5.5e-83;
Matches 184; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
              ||||||||:
Db       1184 IPGLKRKAE 1192
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RESULT 9
US-10-267-502-429
; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416

```
;  CURRENT APPLICATION NUMBER: US/10/267,502
;  CURRENT FILING DATE:  2003-01-27
;  NUMBER OF SEQ ID NOS: 439
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-267-502-429

  Query Match             98.2%;  Score 908;  DB 12;  Length 1192;
  Best Local Similarity   97.4%;  Pred. No. 5.5e-83;
  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
              |||||||:
Db       1184 IPGLKRKAE 1192


RESULT 10
US-10-060-036-71
; Sequence 71, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Persing, David H.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Jiang, Yuqiu
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.566
;  CURRENT APPLICATION NUMBER: US/10/060,036
;  CURRENT FILING DATE:  2002-01-30
;  NUMBER OF SEQ ID NOS: 4560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-060-036-71

  Query Match             98.2%;  Score 908;  DB 14;  Length 1192;
  Best Local Similarity   97.4%;  Pred. No. 5.5e-83;
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  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
              ||||||||:
Db       1184 IPGLKRKAE 1192


RESULT 11
US-10-327-213-9
; Sequence 9, Application US/10327213
; Publication No. US20040121341A1
; GENERAL INFORMATION:
;  APPLICANT: FILBIN, MARIE T.
;  APPLICANT:  DOMENICONI, MARCO
;  APPLICANT:  CAO, ZIXUAN
;  TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)
;  TITLE OF INVENTION:  ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION
;  FILE REFERENCE: CUNY/003
;  CURRENT APPLICATION NUMBER: US/10/327,213
;  CURRENT FILING DATE:  2002-12-20
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-327-213-9

  Query Match             98.2%;  Score 908;  DB 16;  Length 1192;
  Best Local Similarity   97.4%;  Pred. No. 5.5e-83;
  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
```

```
                ||||||||:
Db       1184 IPGLKRKAE 1192


RESULT 12
US-10-466-258-9
; Sequence 9, Application US/10466258
; Publication No. US20040132096A1
; GENERAL INFORMATION:
;  APPLICANT: GLAXO GROUP LIMITED
;  TITLE OF INVENTION: ASSAY
;  FILE REFERENCE: P80966 GCW
;  CURRENT APPLICATION NUMBER: US/10/466,258
;  CURRENT FILING DATE:  2003-07-15
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-466-258-9

  Query Match             98.2%;  Score 908;  DB 16;  Length 1192;
  Best Local Similarity   97.4%;  Pred. No. 5.5e-83;
  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||:|||||||| |||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
              ||||||||:
Db       1184 IPGLKRKAE 1192


RESULT 13
US-10-267-502-431
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
;  APPLICANT: Kim, Jaeseob
;  APPLICANT:  Galant, Ron
;  TITLE OF INVENTION: Obesity Linked Genes
;  FILE REFERENCE: LSD-07416
;  CURRENT APPLICATION NUMBER: US/10/267,502
;  CURRENT FILING DATE:  2003-01-27
;  NUMBER OF SEQ ID NOS: 439
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 431
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; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-267-502-431

Query Match 98.0%; Score 906.5; DB 12; Length 1163;
Best Local Similarity 98.4%; Pred. No. 7.6e-83;
Matches 187; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 59
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        974 SVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 1033

Qy         60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 1093

Qy        120 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 179
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1094 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQA 1153

Qy        180 KIPGLKRKAD 189
              |||||||||:
Db       1154 KIPGLKRKAE 1163
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RESULT 14
US-09-893-348-25
; Sequence 25, Application US/09893348
; Patent No. US20020072493A1
; GENERAL INFORMATION:
; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-348-25

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  Query Match             97.7%;  Score 904;  DB 9;  Length 199;
  Best Local Similarity   97.3%;  Pred. No. 1.3e-83;
  Matches  183;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAD 189
              |||||||:
Db        192 PGLKRKAE 199


RESULT 15
US-10-660-946-1
; Sequence 1, Application US/10660946
; Publication No. US20040063131A1
;   GENERAL INFORMATION:
;        APPLICANT: Bandman, Olga
;                   Au-Young, Janice
;                   Goli, Surya K.
;                   Hillman, Jennifer L.
;        TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
;        NUMBER OF SEQUENCES: 9
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Incyte Pharmaceuticals, Inc.
;             STREET: 3174 Porter Drive
;             CITY: Palo Alto
;             STATE: CA
;             COUNTRY: U.S.
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 1.5
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/660,946
;             FILING DATE: 12-Sep-2003
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/228,213A
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/700,607
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Billings, Lucy J.
;             REGISTRATION NUMBER: 36,749
;             REFERENCE/DOCKET NUMBER: PF-0114 US
;        TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-660-946-1

Query Match 97.7%; Score 904; DB 12; Length 199;
Best Local Similarity 97.3%; Pred. No. 1.3e-83;
Matches 183; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAD 189
              |||||||:
Db        192 PGLKRKAE 199
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Search completed: September 29, 2004, 18:48:12
Job time : 21.2878 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:06:43 ; Search time 14.8689 Seconds
(without alignments)
4010.587 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	917	99.1	578	11	Q80W95	Q80w95 mus musculu
2	917	99.1	639	11	Q8K290	Q8k290 mus musculu
3	917	99.1	1046	11	Q8BGK7	Q8bgk7 mus musculu
4	917	99.1	1162	11	Q8BGM9	Q8bgm9 mus musculu
5	914	98.8	375	11	Q8BHF5	Q8bhf5 mus musculu
6	913	98.7	356	11	Q8BH78	Q8bh78 mus musculu
7	908	98.2	986	4	Q8IUA4	Q8iua4 homo sapien
8	906.5	98.0	1163	11	Q8K3G8	Q8k3g8 mus musculu
9	905	97.8	392	4	Q96B16	Q96b16 homo sapien
10	902.5	97.6	357	11	Q8K3G7	Q8k3g7 mus musculu
11	878	94.9	184	6	Q7YRW9	Q7yrw9 bos taurus
12	872	94.3	199	13	Q7T224	Q7t224 gallus gall
13	844	91.2	179	6	Q9GM33	Q9gm33 macaca fasc
14	733	79.2	214	13	Q7T222	Q7t222 carassius a
15	679	73.4	199	4	Q9BQ59	Q9bq59 homo sapien
16	678	73.3	780	11	Q8K4S4	Q8k4s4 mus musculu
17	678	73.3	780	11	Q8K0T0	Q8k0t0 mus musculu
18	669	72.3	760	13	Q90638	Q90638 gallus gall
19	665	71.9	208	13	Q90637	Q90637 gallus gall
20	665	71.9	267	11	Q63765	Q63765 rattus sp.
21	622.5	67.3	236	11	Q8VBU0	Q8vbu0 rattus norv
22	622.5	67.3	237	11	Q8C6D5	Q8c6d5 mus musculu
23	621.5	67.2	643	11	Q8CCU2	Q8ccu2 mus musculu
24	581	62.8	221	13	Q7ZUD6	Q7zud6 brachydanio
25	521	56.3	224	5	Q9VMW1	Q9vmw1 drosophila
26	520	56.2	222	5	Q9VMW4	Q9vmw4 drosophila
27	520	56.2	234	5	Q9VMW3	Q9vmw3 drosophila
28	520	56.2	595	5	Q9VMV9	Q9vmv9 drosophila
29	518	56.0	202	5	Q9VMW2	Q9vmw2 drosophila
30	344	37.2	107	13	Q7T223	Q7t223 carassius a
31	321	34.7	2484	5	Q9U347	Q9u347 caenorhabdi
32	321	34.7	2607	5	Q23187	Q23187 caenorhabdi
33	320	34.6	222	5	Q23188	Q23188 caenorhabdi
34	198.5	21.5	154	5	Q9VIB7	Q9vib7 drosophila
35	198.5	21.5	158	5	Q24199	Q24199 drosophila
36	194	21.0	255	10	O82352	O82352 arabidopsis
37	189	20.4	255	10	Q9SH59	Q9sh59 arabidopsis
38	182	19.7	271	10	Q9SUT9	Q9sut9 arabidopsis
39	170	18.4	257	10	Q9FFS0	Q9ffs0 arabidopsis
40	163	17.6	275	10	Q9SUR3	Q9sur3 arabidopsis
41	160	17.3	200	10	Q9LT71	Q9lt71 arabidopsis
42	158	17.1	200	10	Q8LAT8	Q8lat8 arabidopsis
43	158	17.1	279	10	Q9AWY7	Q9awy7 oryza sativ
44	154.5	16.7	192	10	Q7XR59	Q7xr59 oryza sativ
45	154	16.6	253	10	Q8S2K0	Q8s2k0 oryza sativ

ALIGNMENTS

RESULT 1
Q80W95
ID Q80W95 PRELIMINARY; PRT; 578 AA.
AC Q80W95;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

```
DE   Nogo-A (Fragment).
GN   NOGO-A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tozaki H., Hirata T.;
RT   "The partial sequence of mouse nogo-A cDNA clone#4109.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB073672; BAC75974.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   578 AA;  63696 MW;  832670C171E4AC61 CRC64;

  Query Match             99.1%;  Score 917;  DB 11;  Length 578;
  Best Local Similarity   98.9%;  Pred. No. 2.5e-72;
  Matches  187;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 449

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 509

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        510 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 569

Qy        181 IPGLKRKAD 189
              |||||||:
Db        570 IPGLKRKAE 578


RESULT 2
Q8K290
ID   Q8K290      PRELIMINARY;      PRT;   639 AA.
AC   Q8K290;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
```

```
DR   EMBL; BC032192; AAH32192.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   639 AA;  70312 MW;  309A19DA37603F11 CRC64;

  Query Match             99.1%;  Score 917;  DB 11;  Length 639;
  Best Local Similarity   98.9%;  Pred. No. 2.8e-72;
  Matches  187;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 510

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 570

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        571 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 630

Qy        181 IPGLKRKAD 189
              ||||||||:
Db        631 IPGLKRKAE 639


RESULT 3
Q8BGK7
ID   Q8BGK7      PRELIMINARY;      PRT;  1046 AA.
AC   Q8BGK7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
```

```
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102280; AAM73502.1; -.
DR   EMBL; AY102286; AAM73507.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1046 AA;  114221 MW;  8CE2E2238ED51222 CRC64;

  Query Match             99.1%;  Score 917;  DB 11;  Length 1046;
  Best Local Similarity   98.9%;  Pred. No. 4.9e-72;
  Matches  187;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 917

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 977

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        978 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 1037

Qy        181 IPGLKRKAD 189
              |||||||:
Db       1038 IPGLKRKAE 1046


RESULT 4
Q8BGM9
ID   Q8BGM9      PRELIMINARY;      PRT;  1162 AA.
AC   Q8BGM9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
```

```
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102284; AAM73506.1; -.
DR   EMBL; AY102286; AAM73511.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1162 AA;  126613 MW;  855697FBEE11781F CRC64;

  Query Match             99.1%;  Score 917;  DB 11;  Length 1162;
  Best Local Similarity   98.9%;  Pred. No. 5.5e-72;
  Matches  187;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        974 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1033

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1093

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1094 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 1153

Qy        181 IPGLKRKAD 189
              |||||||||:
Db       1154 IPGLKRKAE 1162


RESULT 5
Q8BHF5
ID   Q8BHF5      PRELIMINARY;      PRT;   375 AA.
AC   Q8BHF5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
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GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102282; AAM73504.1; -.
DR   EMBL; AY102286; AAM73509.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   375 AA;  40300 MW;  23D9EB19BE671AE6 CRC64;

  Query Match             98.8%;  Score 914;  DB 11;  Length 375;
  Best Local Similarity   98.4%;  Pred. No. 2.8e-72;
  Matches  186;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 246

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 306

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        307 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 366

Qy        181 IPGLKRKAD 189
              ||||||||:
Db        367 IPGLKRKAE 375
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RESULT 6
Q8BH78
ID   Q8BH78      PRELIMINARY;      PRT;   356 AA.
AC   Q8BH78;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7, and 129SvcJ7;
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvcJ7;
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129SvcJ7;
RA   Van der Putten H., Mir A.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY102281; AAM73503.1; -.
DR   EMBL; AY102286; AAM73508.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   356 AA;  38403 MW;  4366C03BA9630B56 CRC64;

  Query Match           98.7%;  Score 913;  DB 11;  Length 356;
  Best Local Similarity  98.9%;  Pred. No. 3.3e-72;
  Matches  186;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 228

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 288
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Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        289 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKI 348

Qy        182 PGLKRKAD 189
              |||||||:
Db        349 PGLKRKAE 356
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RESULT 7
Q8IUA4
ID   Q8IUA4      PRELIMINARY;      PRT;   986 AA.
AC   Q8IUA4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   RNT4 (RTN4).
GN   RTN4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22376540; PubMed=12488097;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   J. Mol. Biol. 325:299-323(2003).
DR   EMBL; AY102285; AAM64244.1; -.
DR   EMBL; AY123245; AAM64249.1; -.
DR   EMBL; AY123246; AAM64250.1; -.
DR   EMBL; AY123247; AAM64251.1; -.
DR   EMBL; AY123248; AAM64252.1; -.
DR   EMBL; AY123249; AAM64253.1; -.
DR   EMBL; AY123250; AAM64254.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   986 AA;  108449 MW;  0CDE8F647036415A CRC64;
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  Query Match             98.2%;  Score 908;  DB 4;  Length 986;
  Best Local Similarity   97.4%;  Pred. No. 2.8e-71;
  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 857

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        858 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 917

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db        918 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 977

Qy        181 IPGLKRKAD 189
              ||||||||:
Db        978 IPGLKRKAE 986


RESULT 8
Q8K3G8
ID   Q8K3G8      PRELIMINARY;      PRT;  1163 AA.
AC   Q8K3G8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-A.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Jin W., Long M., Li R., Ju G.;
RT   "Cloning and expression of the mouse Nogo-A protein.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114152; AAM77068.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   1163 AA;  126691 MW;  6B5F362799417EA4 CRC64;

  Query Match             98.0%;  Score 906.5;  DB 11;  Length 1163;
  Best Local Similarity   98.4%;  Pred. No. 4.6e-71;
  Matches  187;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 SVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 59
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        974 SVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQ 1033
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Qy         60 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1034 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFA 1093

Qy        120 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQA 179
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       1094 VLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQA 1153

Qy        180 KIPGLKRKAD 189
              |||||||||:
Db       1154 KIPGLKRKAE 1163
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RESULT 9
Q96B16
ID   Q96B16      PRELIMINARY;      PRT;   392 AA.
AC   Q96B16;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein (RTN4).
GN   RTN4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Oertle T., Schwab M.E.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Van der Putten H.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22376540; PubMed=12488097;
RA   Oertle T., van der Putten H., Schwab M.E.;
RT   "Genomic Structure and Functional Characterization of the Promoter
RT   Structures of Human and Mouse Nogo/Rtn-4.";
RL   J. Mol. Biol. 325:299-323(2003).
DR   EMBL; BC016165; AAH16165.1; -.
DR   EMBL; AY102285; AAM64242.1; -.
DR   EMBL; AY102278; AAM64247.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
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DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   392 AA;  42274 MW;  D7B2AA5E839E58AD CRC64;

  Query Match             97.8%;  Score 905;  DB 4;  Length 392;
  Best Local Similarity   96.8%;  Pred. No. 1.8e-71;
  Matches  183;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 263

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        264 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 323

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db        324 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 383

Qy        181 IPGLKRKAD 189
              |||||||:
Db        384 IPGLKRKAE 392


RESULT 10
Q8K3G7
ID   Q8K3G7      PRELIMINARY;      PRT;   357 AA.
AC   Q8K3G7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-B.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Jin W., Li R., Long M., Shen J., Ju G.;
RT   "Cloning and expression of the mouse Nogo-B protein.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114153; AAM77069.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   357 AA;  38566 MW;  73BB3D17DFDBDF15 CRC64;

  Query Match             97.6%;  Score 902.5;  DB 11;  Length 357;
  Best Local Similarity   98.4%;  Pred. No. 2.8e-71;
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  Matches  186;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          2 VVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        169 VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 228

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 288

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        289 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAK 348

Qy        181 IPGLKRKAD 189
              ||||||||:
Db        349 IPGLKRKAE 357


RESULT 11
Q7YRW9
ID   Q7YRW9      PRELIMINARY;      PRT;   184 AA.
AC   Q7YRW9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4w (Fragment).
GN   RTN4.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
DR   EMBL; AY164744; AAP47319.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   184 AA;  20671 MW;  DE990E03BBAF84A1 CRC64;

  Query Match             94.9%;  Score 878;  DB 6;  Length 184;
  Best Local Similarity   96.2%;  Pred. No. 1.9e-69;
  Matches  177;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSD 65
              |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSD 60

Qy         66 EGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVF 125
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 EGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVF 120

Qy        126 TYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLK 185
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                    ||||||||||||||||||||||:||||||||  ||||||||||:||||||||||||||||
Db        121 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 180

Qy        186 RKAD 189
                  |||:
Db        181 RKAE 184
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RESULT 12
Q7T224
ID   Q7T224   PRELIMINARY;   PRT;   199 AA.
AC   Q7T224;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4-C.
GN   RTN4.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
DR   EMBL; AY164737; AAP47312.1; -.
SQ   SEQUENCE   199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

  Query Match   94.3%; Score 872; DB 13; Length 199;
  Best Local Similarity   91.5%; Pred. No. 6.9e-69;
  Matches 172; Conservative   10; Mismatches   6; Indels   0; Gaps   0;

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Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||:||:||:|:|||||:  |||:| |:||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESDVAVSEDLIQKYSSVVLGHINGTVKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              |||||||||||||||||||||||||:||||||| |||||||| ||:||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLVNKNVKDAMAKIQAKI 191

Qy        182 PGLKRKAD 189
              |||||| :
Db        192 PGLKRKTE 199
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RESULT 13
Q9GM33
ID   Q9GM33   PRELIMINARY;   PRT;   179 AA.
AC   Q9GM33;

```
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RT   "Isolation of full-length cDNA clones from macaque brain cDNA
RT   libraries.";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB049853; BAB16739.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   179 AA;  19949 MW;  5F8CD4383FEE9E02 CRC64;

  Query Match             91.2%;  Score 844;  DB 6;  Length 179;
  Best Local Similarity   95.5%;  Pred. No. 1.8e-66;
  Matches  171;  Conservative    6;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          11 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPF 70
               :|||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db           1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIQAIQKSDEGHPF 60

Qy          71 RAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGA 130
               |||||||||||||||||||||||| ||||||||||||||||:||||||||||||
Db          61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLRFAVLMWVFTYVGA 120

Qy         131 LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 189
               |||||||||||||||:|||||||| ||||||||||:||||||||||||||||||||:
Db         121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179


RESULT 14
Q7T222
ID   Q7T222      PRELIMINARY;      PRT;   214 AA.
AC   Q7T222;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RTN4-M.
GN   RTN4.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
DR   EMBL; AY164754; AAP47329.1; -.
SQ   SEQUENCE   214 AA;  24063 MW;  E9B603B043159DD9 CRC64;

  Query Match             79.2%;  Score 733;  DB 13;  Length 214;
  Best Local Similarity   73.4%;  Pred. No. 1.3e-56;
  Matches  138;  Conservative   25;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              |||||||||:::|||||||| |||||:| ||:|| :|:||||||||||||||||::||:
Db         27 VVDLLYWRDLQRTGVVFGASLLLLLSLSVCSIISVISYVALALLSVTISFRIYKGILQAV 86

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              |||::|||||: ||: :: || |||||||::|| |:|  ||||||||||:||||||||||
Db         87 QKSEDGHPFKMYLDKDIGISSELVQKYSDTALAHINCVIKELRRLFLVEDLVDSLKFAVF 146

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              ||: |||||||||||||: ||  || |||||:|| ||||| || || :|| | ||||||
Db        147 MWILTYVGALFNGLTLLIMGLIGTFSWPVIYEKHQAQIDHYYGLVNKQIKDVMGKIQAKI 206

Qy        182 PGLKRKAD 189
              || | | :
Db        207 PGAKPKTE 214


RESULT 15
Q9BQ59
ID   Q9BQ59      PRELIMINARY;      PRT;   199 AA.
AC   Q9BQ59;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to reticulon 1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003003; AAH03003.1; -.
DR   EMBL; BC000314; AAH00314.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   GO; GO:0000786; C:nucleosome; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.
DR   GO; GO:0006334; P:nucleosome assembly; IEA.
DR   InterPro; IPR001951; Histone_H4.
DR   InterPro; IPR003388; Reticulon.
```

DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00047; HISTONE_H4; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

  Query Match 73.4%; Score 679; DB 4; Length 199;
  Best Local Similarity 67.9%; Pred. No. 6.6e-52;
  Matches 127; Conservative 31; Mismatches 29; Indels 0; Gaps 0;

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Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db         13 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 72

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
              |:||||||:|||| |: :|:| :|||::    :||||:||||||||| ||||||||||||
Db         73 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 132

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|| ||| ||||    :   :||||||||
Db        133 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 192

Qy        183 GLKRKAD 189
              | || |:
Db        193 GAKRHAE 199
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Search completed: September 29, 2004, 18:19:40
Job time : 15.8689 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:04:48 ; Search time 2.70944 Seconds
(without alignments)
3632.211 Million cell updates/sec

Title: US-09-830-972-2_COPY_975_1163
Perfect score: 925
Sequence: 1 SVVDLLYWRDIKKTGVVFGA.....VKDAMAKIQAKIPGLKRKAD 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	925	100.0	1163	1	RTN4_RAT	Q9jk11 rattus norv
2	913	98.7	199	1	RTN4_MOUSE	Q99p72 mus musculu
3	908	98.2	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
4	679	73.4	776	1	RTN1_HUMAN	Q16799 homo sapien
5	678	73.3	777	1	RTN1_RAT	Q64548 rattus norv
6	622.5	67.3	236	1	RTN3_HUMAN	O95197 homo sapien
7	622.5	67.3	237	1	RTN3_MOUSE	Q9es97 mus musculu
8	475	51.4	545	1	RTN2_HUMAN	O75298 homo sapien
9	472	51.0	471	1	RTN2_MOUSE	O70622 mus musculu
10	94	10.2	468	1	ACH5_HUMAN	P30532 homo sapien
11	92.5	10.0	197	1	AR61_DROME	Q9ves1 drosophila
12	88.5	9.6	1278	1	NPC1_HUMAN	O15118 homo sapien
13	86.5	9.4	578	1	MDLB_BUCBP	Q89a96 buchnera ap
14	86	9.3	589	1	Y015_MYCGE	P47261 mycoplasma
15	85.5	9.2	296	1	YBZ7_YEAST	P38279 saccharomyc
16	85	9.2	299	1	Y779_METJA	Q58189 methanococc
17	83.5	9.0	570	1	SECD_STRCO	Q53955 streptomyce

18	83	9.0	388	1	YUBA_BACSU	O32086 bacillus su
19	82.5	8.9	502	1	OXAA_AQUAE	O66561 aquifex aeo
20	82	8.9	744	1	PRES_RAT	Q9eph0 rattus norv
21	81.5	8.8	499	1	UBPG_YEAST	Q02863 saccharomyc
22	81.5	8.8	580	1	MDLB_BUCAI	P57552 buchnera ap
23	81.5	8.8	839	1	TLR4_PANPA	Q9ttn0 pan paniscu
24	81	8.8	607	1	GLMS_AGRT5	Q8ueh1 a glucosami
25	81	8.8	744	1	PRES_MERUN	Q9jkq2 meriones un
26	81	8.8	744	1	PRES_MOUSE	Q99nh7 mus musculu
27	79.5	8.6	324	1	MRAY_LISIN	Q929y0 listeria in
28	79.5	8.6	470	1	YMP8_CAEEL	P53993 caenorhabdi
29	79.5	8.6	592	1	Y036_HAEIN	Q57335 haemophilus
30	79	8.5	556	1	NU2M_PODAN	P15578 podospora a
31	78.5	8.5	748	1	TAP1_HUMAN	Q03518 homo sapien
32	78	8.4	284	1	HTPX_METJA	Q59076 methanococc
33	78	8.4	660	1	SGAT_MYCPN	P75291 mycoplasma
34	78	8.4	744	1	PRES_HUMAN	P58743 homo sapien
35	78	8.4	993	1	NISB_LACLA	P20103 lactococcus
36	77.5	8.4	503	1	C72R_ARATH	Q9sae1 arabidopsis
37	77.5	8.4	780	1	FTSK_SPOUR	Q9rnv1 sporosarcin
38	77.5	8.4	1277	1	NPC1_PIG	P56941 sus scrofa
39	77	8.3	329	1	O5T2_HUMAN	Q8ngg2 homo sapien
40	77	8.3	839	1	TLR4_HUMAN	O00206 homo sapien
41	76.5	8.3	526	1	ERGL_HUMAN	Q9hat1 homo sapien
42	76	8.2	312	1	OLF2_CHICK	P37068 gallus gall
43	76	8.2	666	1	NU5M_CHOCR	P48920 chondrus cr
44	75.5	8.2	221	1	YA78_AQUAE	O67171 aquifex aeo
45	75.5	8.2	554	1	PIGS_HUMAN	Q96s52 homo sapien

ALIGNMENTS

```
RESULT 1
RTN4_RAT
ID   RTN4_RAT       STANDARD;      PRT;  1163 AA.
AC   Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE   (Glut4 vesicle 20 kDa protein).
GN   RTN4 OR NOGO.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Adipocyte;
RX   MEDLINE=99249816; PubMed=10231557;
RA   Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;
RT   "Cloning and characterization of a 22 kDa protein from rat adipocytes:
RT   a new member of the reticulon family.";
RL   Biochim. Biophys. Acta 1450:68-76(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
```

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RX   MEDLINE=20129258; PubMed=10667796;
RA   Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
RA   Spillmann A.A., Christ F., Schwab M.E.;
RT   "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
RT   antigen for monoclonal antibody IN-1.";
RL   Nature 403:434-439(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
RC   STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
RA   Ito T., Schwartz S.M.;
RT   "Cloning of a member of the reticulon gene family in rat: one of two
RT   minor splice variants.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   FUNCTION.
RX   MEDLINE=22033691; PubMed=12037567;
RA   GrandPre T., Li S., Strittmatter S.M.;
RT   "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
RL   Nature 417:547-551(2002).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults (By
CC       similarity).
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC       membrane of the endoplasmic reticulum through 2 putative
CC       transmembrane domains (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=Nogo-A, NI-220-250;
CC         IsoId=Q9JK11-1; Sequence=Displayed;
CC       Name=2; Synonyms=Nogo-B, Foocen-M1;
CC         IsoId=Q9JK11-2; Sequence=VSP_005658;
CC       Name=3; Synonyms=Nogo-C, VP20;
CC         IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
CC       Name=4; Synonyms=Foocen-M2;
CC         IsoId=Q9JK11-4; Sequence=VSP_005659;
CC   -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
CC       nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
CC       present in dorsal root ganglion, sciatic nerve and PC12 cells
CC       after longer exposure. Isoforms 2 and 3 are detected in kidney,
CC       cartilage, skin, lung and spleen. Isoform 3 is expressed at high
CC       level in skeletal muscle. In adult animals isoform 1 is expressed
CC       mainly in the nervous system.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF051335; AAF01564.1; -.
DR   EMBL; AJ242961; CAB71027.1; -.
DR   EMBL; AJ242962; CAB71028.1; -.
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DR   EMBL; AJ242963; CAB71029.1; -.
DR   EMBL; AF132045; AAD31019.1; -.
DR   EMBL; AF132046; AAD31020.1; -.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
DR   GO; GO:0005635; C:nuclear membrane; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR   GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   DOMAIN        1    989       CYTOPLASMIC (Potential).
FT   TRANSMEM    990   1010       POTENTIAL.
FT   DOMAIN     1011   1104       LUMENAL (Potential).
FT   TRANSMEM   1105   1125       POTENTIAL.
FT   DOMAIN     1126   1163       CYTOPLASMIC (Potential).
FT   DOMAIN      976   1163       RETICULON.
FT   DOMAIN       33     46       POLY-GLU.
FT   DOMAIN       73     76       POLY-ALA.
FT   DOMAIN      140    145       POLY-PRO.
FT   VARSPLIC      1    964       Missing (in isoform 3).
FT                                /FTId=VSP_005656.
FT   VARSPLIC    965    975       AVLSAELSKTS -> MDGQKKHWKDK (in isoform
FT                                3).
FT                                /FTId=VSP_005657.
FT   VARSPLIC    173    975       Missing (in isoform 2).
FT                                /FTId=VSP_005658.
FT   VARSPLIC    192    975       Missing (in isoform 4).
FT                                /FTId=VSP_005659.
FT   CONFLICT   1130   1131       MISSING (IN REF. 3; AAD31020).
SQ   SEQUENCE   1163 AA;  126386 MW;  8CB894B09E94F0B6 CRC64;

  Query Match             100.0%;  Score 925;  DB 1;  Length 1163;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-68;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        975 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1034

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1035 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 1094

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1095 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154

Qy        181 IPGLKRKAD 189
              |||||||||
Db       1155 IPGLKRKAD 1163


RESULT 2
RTN4_MOUSE
ID   RTN4_MOUSE     STANDARD;      PRT;   199 AA.
```

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AC   Q99P72; Q9CTE3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).
GN   RTN4 OR NOGO.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3T3-L1; TISSUE=Adipocyte;
RA   Coulson A.C., Craggs P.D., Morris N.J.;
RT   "Mouse vp20/RTN4C cDNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 170-199 FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults (By
CC       similarity).
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
CC       membrane of the endoplasmic reticulum through 2 putative
CC       transmembrane domains (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms may be produced;
CC       Name=1;
CC         IsoId=Q99P72-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF326337; AAK08076.1; -.
DR   EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
DR   GO; GO:0005635; C:nuclear membrane; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR   GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   DOMAIN        1     25       CYTOPLASMIC (Potential).
FT   TRANSMEM     26     50       POTENTIAL.
FT   DOMAIN       51    137       LUMENAL (Potential).
FT   TRANSMEM    138    162       POTENTIAL.
FT   DOMAIN      163    199       CYTOPLASMIC (Potential).
FT   DOMAIN       12    199       RETICULON.
SQ   SEQUENCE   199 AA;  22466 MW;  07BE5D580059ED9C CRC64;

  Query Match             98.7%;  Score 913;  DB 1;  Length 199;
  Best Local Similarity   98.9%;  Pred. No. 2e-68;
  Matches  186;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         12 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 71

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 131

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        132 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKI 191

Qy        182 PGLKRKAD 189
              |||||||:
Db        192 PGLKRKAE 199


RESULT 3
RTN4_HUMAN
ID   RTN4_HUMAN     STANDARD;      PRT;  1192 AA.
AC   Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC   Q9Y5U6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
```

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN RTN4 OR NOGO OR ASY OR KIAA0886.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129242; PubMed=10667780;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans.";
RL Nature 403:383-384(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=21010696; PubMed=11126360;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
RT 2p14-->2p13 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 88:101-102(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;
RT "Isolation of a cell death-inducing gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Pituitary;
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
RA Luo B., Hu R., Chen J.;
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,

RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clone with function of inhibiting cancer cell
RT growth.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560(2000).
RN [12]
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
RC TISSUE=Brain;
RA Mao Y.M., Xie Y., Zheng Z.H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN [13]
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;

```
RA   Sha J.H., Zhou Z.M., Li J.M.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [14]
RP   TOPOLOGY.
RC   TISSUE=Brain;
RX   MEDLINE=20129259; PubMed=10667797;
RA   GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
RT   "Identification of the Nogo inhibitor of axon regeneration as a
RT   Reticulon protein.";
RL   Nature 403:439-444(2000).
RN   [15]
RP   FUNCTION.
RC   TISSUE=Brain;
RX   MEDLINE=21069055; PubMed=11201742;
RA   Fournier A.E., Grandpre T., Strittmatter S.M.;
RT   "Identification of a receptor mediating Nogo-66 inhibition of axonal
RT   regeneration.";
RL   Nature 409:341-346(2001).
RN   [16]
RP   REVIEW.
RX   MEDLINE=21888956; PubMed=11891768;
RA   Ng C.E.L., Tang B.L.;
RT   "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
RT   regeneration.";
RL   J. Neurosci. Res. 67:559-565(2002).
CC   -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
CC       block the regeneration of the nervous central system in adults.
CC       Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
CC       This is likely consecutive to their change in subcellular
CC       location, from the mitochondria to the endoplasmic reticulum,
CC       after binding and sequestration.
CC   -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum. Anchored to the membrane of the endoplasmic reticulum
CC       through 2 putative transmembrane domains.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
CC         IsoId=Q9NQC3-1; Sequence=Displayed;
CC       Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
CC         IsoId=Q9NQC3-2; Sequence=VSP_005655;
CC       Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
CC         IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
CC       Name=4;
CC         IsoId=Q9NQC3-4; Sequence=VSP_005654;
CC   -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain
CC       and testis and weakly in heart and skeletal muscle. Isoform 2 is
CC       widely expressed excepted for the liver. Isoform 3 is expressed in
CC       brain, skeletal muscle and adipocytes. Isoform 4 is testis-
CC       specific.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   -!- CAUTION: Ref.11 sequence differs from that shown due to
CC       frameshifts in positions 1149 and 1156.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ251383; CAB99248.1; -.
DR   EMBL; AJ251384; CAB99249.1; -.
DR   EMBL; AJ251385; CAB99250.1; -.
DR   EMBL; AB040462; BAB18927.1; -.
DR   EMBL; AB040463; BAB18928.1; -.
DR   EMBL; AF148537; AAG12176.1; -.
DR   EMBL; AF148538; AAG12177.1; -.
DR   EMBL; AF087901; AAG12205.1; -.
DR   EMBL; AF320999; AAG40878.1; -.
DR   EMBL; AF132047; AAD31021.1; -.
DR   EMBL; AF132048; AAD31022.1; -.
DR   EMBL; AB015639; BAA83712.1; -.
DR   EMBL; AF077050; AAD27783.1; -.
DR   EMBL; AF177332; AAG17976.1; -.
DR   EMBL; AB020693; BAA74909.1; -.
DR   EMBL; BC001035; AAH01035.1; -.
DR   EMBL; BC007109; AAH07109.1; -.
DR   EMBL; BC014366; AAH14366.1; -.

  Query Match             98.2%;  Score 908;  DB 1;  Length 1192;
  Best Local Similarity   97.4%;  Pred. No. 3.2e-67;
  Matches  184;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 1063

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1064 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFAV 1123

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
              |||||||||||||||||||||||||:|||||||| ||||||||||:||||||||||
Db       1124 LMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1183

Qy        181 IPGLKRKAD 189
              ||||||||:
Db       1184 IPGLKRKAE 1192


RESULT 4
RTN1_HUMAN
ID   RTN1_HUMAN     STANDARD;      PRT;   776 AA.
AC   Q16799; Q16800; Q16801;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon 1 (Neuroendocrine-specific protein).
GN   RTN1 OR NSP.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).
RC   TISSUE=Lung carcinoma;
RX   MEDLINE=93293865; PubMed=7685762;
RA   Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,
RA   Ramaekers F.C.S., Van de Ven W.J.M.;
RT   "Cloning and expression of alternative transcripts of a novel
RT   neuroendocrine-specific gene and identification of its 135-kDa
RT   translational product.";
RL   J. Biol. Chem. 268:13439-13447(1993).
RN   [2]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=96429995; PubMed=8833145;
RA   Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,
RA   Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;
RT   "Genomic organization of the human NSP gene, prototype of a novel gene
RT   family encoding reticulons.";
RL   Genomics 32:191-199(1996).
RN   [3]
RP   TISSUE SPECIFICITY.
RX   MEDLINE=98228245; PubMed=9560466;
RA   Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,
RA   Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;
RT   "Neuronal differentiation is accompanied by NSP-C expression.";
RL   Cell Tissue Res. 292:229-237(1998).
CC   -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC       membrane trafficking in neuroendocrine cells.
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=RTN1-A; Synonyms=NSP-A;
CC         IsoId=Q16799-1; Sequence=Displayed;
CC       Name=RTN1-B; Synonyms=NSP-B;
CC         IsoId=Q16799-2; Sequence=VSP_005644;
CC       Name=RTN1-C; Synonyms=NSP-C;
CC         IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
CC       AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
CC       IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
CC   -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L10333; AAA59950.1; -.
DR   EMBL; L10334; AAA59951.1; -.
DR   EMBL; L10335; AAA59952.1; -.
DR   PIR; A46583; A46583.
DR   PIR; I60904; I60904.
DR   Genew; HGNC:10467; RTN1.
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DR   MIM; 600865; -.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
DR   GO; GO:0004871; F:signal transducer activity; NAS.
DR   GO; GO:0030182; P:neuron differentiation; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW   Phosphorylation.
FT   TRANSMEM    603    623       POTENTIAL.
FT   TRANSMEM    726    746       POTENTIAL.
FT   DOMAIN      589    776       RETICULON.
FT   DOMAIN      609    612       POLY-LEU.
FT   VARSPLIC      1    420       Missing (in isoform RTN1-B).
FT                                /FTId=VSP_005644.
FT   VARSPLIC      1    568       Missing (in isoform RTN1-C).
FT                                /FTId=VSP_005645.
FT   VARSPLIC    569    588       GPGPLGPGAPPPLLFLNKQK -> MQATADSTKMDCVWSNW
FT                                KSQ (in isoform RTN1-C).
FT                                /FTId=VSP_005646.
SQ   SEQUENCE   776 AA;  83617 MW;  CA5B6232353096FE CRC64;

  Query Match             73.4%;  Score 679;  DB 1;  Length 776;
  Best Local Similarity   67.9%;  Pred. No. 1.6e-48;
  Matches  127;  Conservative   31;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        590 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQ 649

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :||||:|||||||| ||||||||||
Db        650 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKFAVLM 709

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
              |: |||||||||||||::|::|:|::||:| :|| ||| |||| :  :||||||||
Db        710 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIP 769

Qy        183 GLKRKAD 189
              | || |:
Db        770 GAKRHAE 776


RESULT 5
RTN1_RAT
ID   RTN1_RAT       STANDARD;      PRT;   777 AA.
AC   Q64548; Q64547;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
GN   RTN1 OR NSP.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
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RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC   STRAIN=Wistar; TISSUE=Brain cortex;
RX   MEDLINE=96386034; PubMed=8793864;
RA   Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA   Georgiev G.P., Buchman V.L.;
RT   "Intracellular compartmentalization of two differentially spliced s-
RT   rex/NSP mRNAs in neurons.";
RL   Mol. Cell. Neurosci. 7:289-303(1996).
CC   -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC       membrane trafficking in neuroendocrine cells.
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
CC       similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=RTN1-B; Synonyms=S-RexB;
CC         IsoId=Q64548-1; Sequence=Displayed;
CC       Name=RTN1-S; Synonyms=S-RexS;
CC         IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC       PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC       HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC       EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC       TYPES.
CC   -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC       HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC       DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC       THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC       DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC       HINDBRAIN.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U17604; AAC53046.1; -.
DR   EMBL; U17603; AAC53045.1; -.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   TRANSMEM    604    624       POTENTIAL.
FT   TRANSMEM    727    747       POTENTIAL.
FT   DOMAIN      590    777       RETICULON.
FT   DOMAIN      610    613       POLY-LEU.
FT   VARSPLIC      1    569       Missing (in isoform RTN1-S).
FT                                /FTId=VSP_005647.
FT   VARSPLIC    570    589       IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW
FT                                KSQ (in isoform RTN1-S).
FT                                /FTId=VSP_005648.
SQ   SEQUENCE   777 AA;  83001 MW;  AF7479C50F28D0AC CRC64;
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  Query Match             73.3%;  Score 678;  DB 1;  Length 777;
  Best Local Similarity   67.4%;  Pred. No. 1.9e-48;
  Matches  126;  Conservative   32;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              :|||||||||:||:|||: | || ||| ||:||| ||:||| || |||||||| |:||:|
Db        591 IDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAAALSATISFRIYKSVLQAVQ 650

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVLM 122
              |:|||||:|||| |: :|:| :|||::    :||||:|||||||| ||||||||||||
Db        651 KTDEGHPFKAYLELEITLSQEQIQKYTDCLQLYVNSTLKELRRLFLVQDLVDSLKFAVLM 710

Qy        123 WVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIP 182
              |: ||||||||||||::|::|:|::||:| :|| |:| |||| :  :|||||||
Db        711 WLLTYVGALFNGLTLLLMAVVSMFTLPVVYVKHQAQVDQYLGLVRTHINTVVAKIQAKIP 770

Qy        183 GLKRKAD 189
              | || |:
Db        771 GAKRHAE 777


RESULT 6
RTN3_HUMAN
ID   RTN3_HUMAN     STANDARD;      PRT;   236 AA.
AC   O95197;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
DE   protein II) (NSPLII).
GN   RTN3 OR NSPL2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC   TISSUE=Retina;
RX   MEDLINE=99265974; PubMed=10331947;
RA   Moreira E.F., Jaworski C.J., Rodriguez I.R.;
RT   "Cloning of a novel member of the reticulon gene family (RTN3): gene
RT   structure and chromosomal localization to 11q13.";
RL   Genomics 58:73-81(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
RT   "Cloning and expression analysis of a cDNA encoding a novel
RT   neuroendocrine-specific protein-like protein 1: NSPL1.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, Eye, and Lymph;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
CC       BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
CC       RETINA.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF059524; AAC99319.1; -.
DR   EMBL; AF059529; AAD20951.1; -.
DR   EMBL; AF059525; AAD20951.1; JOINED.
DR   EMBL; AF059526; AAD20951.1; JOINED.
DR   EMBL; AF059527; AAD20951.1; JOINED.
DR   EMBL; AF059528; AAD20951.1; JOINED.
DR   EMBL; AF119297; AAD26810.1; -.
DR   EMBL; BC000634; AAH00634.1; -.
DR   EMBL; BC010556; AAH10556.1; -.
DR   EMBL; BC011394; AAH11394.1; -.
DR   EMBL; BC022993; AAH22993.1; -.
DR   Genew; HGNC:10469; RTN3.
DR   MIM; 604249; -.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Transmembrane; Endoplasmic reticulum.
FT   TRANSMEM     68     88       POTENTIAL.
FT   TRANSMEM    177    197       POTENTIAL.
FT   DOMAIN       48    236       RETICULON.
SQ   SEQUENCE   236 AA;  25609 MW;  DDC6A4544ABCDFB7 CRC64;

  Query Match             67.3%;  Score 622.5;  DB 1;  Length 236;
  Best Local Similarity   59.5%;  Pred. No. 2.1e-44;
  Matches  113;  Conservative   41;  Mismatches   35;  Indels    1;  Gaps    1;
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Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :| ||::|||:|||| ||| :| :|||| ||::|| :|: ||||||||||||| ||||
Db         47 AVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQA 106

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              :|||:|||||:|||: :: :| |    | |:|: |:|  :| : |||||:|||||| ||
Db        107 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDSLKLAV 166

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
               ||: |||||:|||:|||||| : :||:|::||::: |||||:|:|    | : |||||
Db        167 FMWLMTYVGAVFNGITLLILAELLIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 226

Qy        181 IPGL-KRKAD 189
              :||: |:||:
Db        227 LPGIAKKKAE 236
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RESULT 7
RTN3_MOUSE
ID   RTN3_MOUSE     STANDARD;      PRT;   237 AA.
AC   Q9ES97;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Reticulon protein 3.
GN   RTN3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
RT   "Cloning and expression profile of a novel mouse cDNA encoding a human
RT   RTN3 homolog.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
```

```
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF195940; AAG31360.1; -.
DR   EMBL; BC014697; AAH14697.1; -.
DR   MGD; MGI:1339970; Rtn3.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Transmembrane; Endoplasmic reticulum.
FT   TRANSMEM     69     89       POTENTIAL.
FT   TRANSMEM    167    187       POTENTIAL.
FT   DOMAIN       49    237       RETICULON.
SQ   SEQUENCE   237 AA;  25428 MW;  EB60A0A7AC45F0DE CRC64;

  Query Match             67.3%;  Score 622.5;  DB 1;  Length 237;
  Best Local Similarity   59.5%;  Pred. No. 2.1e-44;
  Matches  113;  Conservative   41;  Mismatches   35;  Indels    1;  Gaps    1;

Qy          1 SVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 60
              :| ||::|||:|||| ||| :| :|||| ||::|| :|: |||||||||||:|| ||||
Db         48 AVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRVYKSVIQA 107

Qy         61 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAV 120
              :|||:|||||:|||: :: :| |    | |:|: |||  :| : |||||:||||||| ||
Db        108 VQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHVNKALKLIIRLFLVEDLVDSLKLAV 167

Qy        121 LMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAK 180
               ||: |||||:|||:|||||| : :||:|::||::: |||||:|:|    | : |||||
Db        168 FMWLMTYVGAVFNGITLLILAELLVFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAK 227

Qy        181 IPGL-KRKAD 189
              :||: |:||:
Db        228 LPGIAKKKAE 237


RESULT 8
RTN2_HUMAN
ID   RTN2_HUMAN     STANDARD;      PRT;   545 AA.
AC   O75298; O60509;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
```

```
DE   protein 1) (NSPLI).
GN   RTN2 OR NSPL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC   TISSUE=Lung carcinoma;
RX   MEDLINE=98360096; PubMed=9693037;
RA   Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
RT   "cDNA cloning, genomic organization, and expression of the human RTN2
RT   gene, a member of a gene family encoding reticulons.";
RL   Genomics 51:98-106(1998).
RN   [2]
RP   SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
RC   TISSUE=Brain;
RX   MEDLINE=98191726; PubMed=9530622;
RA   Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT   "Molecular cloning of a novel mouse gene with predominant muscle and
RT   neural expression.";
RL   Mamm. Genome 9:274-282(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC       reticulum (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=RTN2-A;
CC         IsoId=O75298-1; Sequence=Displayed;
CC         Note=Isoform RTN2-C is produced by alternative initiation at
CC         Met-341 of isoform RTN2-A;
CC       Name=RTN2-B;
CC         IsoId=O75298-2; Sequence=VSP_005649;
CC       Event=Alternative initiation;
CC         Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
CC         by alternative initiation at Met-1 and Met-341;
CC   -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
CC       MUSCLE.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF004222; AAC32542.1; -.
DR   EMBL; AF004223; AAC32543.1; -.
DR   EMBL; AF004224; AAC32544.1; -.
DR   EMBL; AF038540; AAC14910.1; -.
DR   Genew; HGNC:10468; RTN2.
DR   MIM; 603183; -.
DR   GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.
DR   GO; GO:0004871; F:signal transducer activity; NAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003388; Reticulon.
```

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DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane;
KW   Alternative initiation.
FT   CHAIN         1    545       RETICULON PROTEIN 2, ISOFORM RTN2-A.
FT   CHAIN       341    545       RETICULON PROTEIN 2, ISOFORM RTN2-C.
FT   INIT_MET    341    341       FOR ISOFORM RTN2-C.
FT   TRANSMEM    368    388       POTENTIAL.
FT   TRANSMEM    463    483       POTENTIAL.
FT   DOMAIN      345    545       RETICULON.
FT   VARSPLIC    272    344       Missing (in isoform RTN2-B).
FT                                /FTId=VSP_005649.
SQ   SEQUENCE   545 AA;  59263 MW;  971FD2F909E1E9E6 CRC64;

  Query Match             51.4%;  Score 475;  DB 1;  Length 545;
  Best Local Similarity   50.5%;  Pred. No. 7e-32;
  Matches   92;  Conservative   36;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              | |||||:| : :|||| : || | |||||| |::|| || ||| |:|: |:||:
Db        345 VADLLYWKDTRTSGVVFTGLMVSLLCLLHFSIVSVAAHLALLLLCGTISLRVYRKVLQAV 404

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
               : |  :||:|||: :: :: |  :: |:     | |   :||  |||:|||||| |:|
Db        405 HRGDGANPFQAYLDVDLTLTREQTERLSHQITSRVVSAATQLRHFFLVEDLVDSLKLALL 464

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
             :: |:|||:|||||||| :| ||:||::| :|| ||| |:||    :    |||:|||
Db        465 FYILTFVGAIFNGLTLLILGVIGLFTIPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKI 524

Qy        182 PG 183
             ||
Db        525 PG 526


RESULT 9
RTN2_MOUSE
ID   RTN2_MOUSE     STANDARD;      PRT;   471 AA.
AC   O70622; O70620;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like
DE   protein 1) (NSPLI).
GN   RTN2 OR NSPL1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
RC   STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
RX   MEDLINE=98191726; PubMed=9530622;
RA   Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
RT   "Molecular cloning of a novel mouse gene with predominant muscle and
RT   neural expression.";
RL   Mamm. Genome 9:274-282(1998).
```

```
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
CC       (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1; Synonyms=Brain;
CC         IsoId=O70622-1; Sequence=Displayed;
CC       Name=2; Synonyms=Muscle;
CC         IsoId=O70622-2; Sequence=VSP_005650, VSP_005651;
CC   -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular
CC       tissues.
CC   -!- SIMILARITY: Contains 1 reticulon domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF038537; AAC14906.1; -.
DR   EMBL; AF038537; AAC14907.1; -.
DR   EMBL; AF038538; AAC14908.1; -.
DR   EMBL; AF038539; AAC14909.1; -.
DR   EMBL; AF093624; AAD13195.1; -.
DR   EMBL; BC031370; AAH31370.1; -.
DR   MGD; MGI:107612; Rtn2.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
KW   Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT   TRANSMEM    295    315       POTENTIAL.
FT   DOMAIN      272    471       RETICULON.
```

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FT   VARSPLIC      1    267       Missing (in isoform 2).
FT                                /FTId=VSP_005650.
FT   VARSPLIC    268    271       PLLL -> MGSK (in isoform 2).
FT                                /FTId=VSP_005651.
SQ   SEQUENCE   471 AA;  51346 MW;  9BBD8F372CF63AD3 CRC64;

  Query Match             51.0%;  Score 472;  DB 1;  Length 471;
  Best Local Similarity   48.9%;  Pred. No. 1.1e-31;
  Matches   89;  Conservative   39;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          2 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 61
              | ||||||:| : :| ||   :  || |  |||||| |::||  |  ||| |:|: |:||:
Db        272 VADLLYWKDTRTSGAVFTGLMASLLCLLHFSIVSVAAHLALLGLCATISLRVYRKVLQAV 331

Qy         62 QKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFAVL 121
               : |  :||:|||: :: :: |  :: |      || ||  :||  |||:|||||| |:|
Db        332 HRGDGTNPFQAYLDMDLTLTREQTERLSQQIASHVVSTATQLRHFFLVEDLVDSLKLALL 391

Qy        122 MWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKI 181
               :: |:|||:|||||||:|| :::||::|::| :|| ||| |:||    :    |||:|||
Db        392 FYILTFVGAIFNGLTLVILGVVALFTVPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKI 451

Qy        182 PG 183
              ||
Db        452 PG 453


RESULT 10
ACH5_HUMAN
ID   ACH5_HUMAN     STANDARD;      PRT;   468 AA.
AC   P30532; Q15824; Q99554;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neuronal acetylcholine receptor protein, alpha-5 chain precursor.
GN   CHRNA5 OR NACHRA5.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92179225; PubMed=1542648;
RA   Chini B., Clementi F., Hukovic N., Sher E.;
RT   "Neuronal-type alpha-bungarotoxin receptors and the alpha 5-nicotinic
RT   receptor subunit gene are expressed in neuronal and nonneuronal human
RT   cell lines.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:1572-1576(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97062879; PubMed=8906617;
RA   Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA   Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT   "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT   2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT   expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT   beta 4 subunits.";
```

RL J. Mol. Neurosci. 7:217-228(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5Y and/or IMR-32.";
RL FEBS Lett. 400:309-314(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Duga S., Solda G., Asselta R., Bonati M.T., Dalpra L., Malcovati M.,
RA Tenchini M.L.;
RT "Characterization of the genomic structure of human nicotinic
RT acetylcholine receptor CHRNA5/A3/B4 gene cluster: identification of
RT two novel introns in the 3' untranslated region of CHRNA3 and of a
RT tail-to-tail overlap between CHRNA3 and CHRNA5.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: After binding acetylcholine, the AChR responds by an
CC extensive change in conformation that affects all subunits and
CC leads to opening of an ion-conducting channel across the plasma
CC membrane.
CC -!- SUBUNIT: Neuronal AChR seems to be composed of two different type
CC of subunits: alpha and non-alpha (betA).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the ligand-gated ionic channel family.
CC ---

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CC   or send an email to license@isb-sib.ch).
CC   ------------------------------------------------------------------------
DR   EMBL; M83712; AAA58357.1; -.
DR   EMBL; U62434; AAB40112.1; -.
DR   EMBL; Y08419; CAA69696.1; -.
DR   EMBL; AJ306481; CAC34820.1; -.
DR   EMBL; AJ306482; CAC34820.1; JOINED.
DR   EMBL; AJ306483; CAC34820.1; JOINED.
DR   EMBL; AJ306484; CAC34820.1; JOINED.
DR   EMBL; AJ306485; CAC34820.1; JOINED.
DR   EMBL; AJ306486; CAC34820.1; JOINED.
DR   EMBL; BC033639; AAH33639.1; -.
DR   PIR; A38223; A38223.
DR   Genew; HGNC:1959; CHRNA5.
DR   MIM; 118505; -.
DR   InterPro; IPR006029; Neu_channel_memb.
DR   InterPro; IPR006202; Neur_chan_LBD.
DR   InterPro; IPR006201; Neur_channel.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   Pfam; PF02932; Neur_chan_memb; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   TIGRFAMs; TIGR00860; LIC; 1.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Multigene family.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    468       NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT                                 ALPHA-5 CHAIN.
FT   DOMAIN       23    249       EXTRACELLULAR.
FT   TRANSMEM    250    274       POTENTIAL.
FT   TRANSMEM    282    299       POTENTIAL.
FT   TRANSMEM    316    337       POTENTIAL.
FT   DOMAIN      338    429       CYTOPLASMIC.
FT   TRANSMEM    430    448       POTENTIAL.
FT   DISULFID    170    184       BY SIMILARITY.
FT   DISULFID    234    235       ASSOCIATED WITH RECEPTOR ACTIVATION
FT                                 (BY SIMILARITY).
FT   CARBOHYD    155    155       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    183    183       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    229    229       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     23     34       RCGLAGAAGGAQ -> ALRSSRARRAAR (IN REF. 1).
FT   CONFLICT    128    128       V -> S (IN REF. 1).
FT   CONFLICT    365    365       C -> S (IN REF. 1).
FT   CONFLICT    398    398       D -> N (IN REF. 2 AND 4).
FT   CONFLICT    405    405       R -> T (IN REF. 1).
SQ   SEQUENCE   468 AA;  53054 MW;  7FE91A2E362289C0 CRC64;

  Query Match             10.2%;  Score 94;  DB 1;  Length 468;
  Best Local Similarity   21.5%;  Pred. No. 1.5;
  Matches   41;  Conservative   32;  Mismatches   62;  Indels   56;  Gaps    7;

Qy         24 LLLSLTVFSIV-------------SVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHP- 69
              :|:|||||| :|              :  |:   :: ||:|  :    |    :|   |
Db        288 VLVSLTVFLLVIEEIIPSSSKVIPLIGEYLVFTMIFVTLSIMVTVFAINIHHRSSSTHNA 347

Qy         70 ------------------FRAYLESEVAISEELVQ----KYSNSALGHVNSTIKELRRLF 107
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                                    |::::      ||       | | : |     :|: : |
Db        348 MAPLVRKIFLHTLPKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALDSIRYITRHI 407

Qy        108 L----VDDLVDSLKF------AVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 157
              :    | ::|:  ||       : :| | :|          |:  : || :||||:   :
Db        408 MKENDVREVVEDWKFIAQVLDRMFLWTFLFVS---------IVGSLGLF-VPVIYKWANI 457

Qy        158 QIDHYLGLANK 168
               |  ::| |||
Db        458 LIPVHIGNANK 468


RESULT 11
AR61_DROME
ID   AR61_DROME     STANDARD;      PRT;   197 AA.
AC   Q9VES1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   ARL-6 interacting protein-1 homolog.
GN   CG10326.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the ARL6ip family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AE003714; AAF55348.1; -.
DR   FlyBase; FBgn0038453; CG10326.
KW   Transmembrane.
FT   TRANSMEM     43     63       POTENTIAL.
FT   TRANSMEM     64     84       POTENTIAL.
FT   TRANSMEM    129    149       POTENTIAL.
FT   TRANSMEM    150    170       POTENTIAL.
SQ   SEQUENCE   197 AA;  22233 MW;  7D35ABAD18CE272E CRC64;

  Query Match             10.0%;  Score 92.5;  DB 1;  Length 197;
  Best Local Similarity   24.6%;  Pred. No. 0.83;
  Matches   48;  Conservative   24;  Mismatches   80;  Indels   43;  Gaps    8;

Qy          5 LLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFR-------IYKGV 57
              :| |      |||||    | | |    :  :|    | ::|: :::        |: ||
Db         32 VLTWEKQYYAGVVFGVISCLYLVLWYLDLSLITLLSLLGVISILLNYAFPMVSRLIFGGV 91

Qy         58 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLK 117
                    |:   |        |:   ||  |          ||:      |::   | ||
Db         92 ---NWDGDQEAKFEDVCGQVCAVKGSLVVWY-EYLFNERKSTV------FVI---VMSLG 138

Qy        118 FAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAK- 176
                : |    :||: | | |: || : :   |              || || :  |: :
Db        139 LLAMAW----IGAIINNLLLMYLATLLILMWP-------------GLQNKDIFKAITQR 180

Qy        177 ----IQAKIPGLKRK 187
                  |  ||   |||
Db        181 ASKIINEKIQCGKRK 195


RESULT 12
NPC1_HUMAN
ID   NPC1_HUMAN     STANDARD;      PRT;  1278 AA.
AC   O15118; Q9P130;
DT   30-MAY-2000 (Rel. 39, Created)
```

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Niemann-Pick C1 protein precursor.
GN NPC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS NPC1.
RX MEDLINE=97362323; PubMed=9211849;
RA Carstea E.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D.,
RA Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B.,
RA Nagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A.,
RA Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R.,
RA Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y.,
RA Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J.,
RA Markie D., O'Neill R.R., van Diggelen O.P., Elleder M.,
RA Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A.;
RT "Niemann-Pick C1 disease gene: homology to mediators of cholesterol
RT homeostasis.";
RL Science 277:228-231(1997).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=99355599; PubMed=10425213;
RA Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
RA Carstea E.D.;
RT "The genomic organization and polymorphism analysis of the human
RT Niemann-Pick C1 gene.";
RL Biochem. Biophys. Res. Commun. 261:493-498(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21623216; PubMed=11754101;
RA Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J.,
RA Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.;
RT "NPC1: Complete genomic sequence, mutation analysis, and
RT characterization of haplotypes.";
RL Hum. Mutat. 19:30-38(2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99128318; PubMed=9927649;
RA Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S.,
RA Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III;
RT "Niemann-Pick C1 protein: obligatory roles for N-terminal domains and
RT lysosomal targeting in cholesterol mobilization.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
RN [5]
RP VARIANT NPD TRP-992.
RX MEDLINE=98299797; PubMed=9634529;
RA Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M.,
RA Byers D.M., Dobson M.J., Neumann P.E.;
RT "The Nova Scotia (type D) form of Niemann-Pick disease is caused by a
RT G3097-->T transversion in NPC1.";
RL Am. J. Hum. Genet. 63:52-54(1998).
RN [6]
RP VARIANTS NPC1 GLN-934; LEU-940; ASN-948; LEU-954; TRP-992; ALA-1007;
RP THR-1061 AND VAL-1213.

RX MEDLINE=99452586; PubMed=10521290;
RA Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C.,
RA Neumann P.E.;
RT "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich
RT domain.";
RL Am. J. Hum. Genet. 65:1252-1260(1999).
RN [7]
RP VARIANT NPC1 THR-1061.
RX MEDLINE=99452593; PubMed=10521297;
RA Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A.,
RA Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.;
RT "Niemann-Pick C1 disease: the I1061T substitution is a frequent mutant
RT allele in patients of Western European descent and correlates with a
RT classic juvenile phenotype.";
RL Am. J. Hum. Genet. 65:1321-1329(1999).
RN [8]
RP VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.
RX MEDLINE=99408226; PubMed=10480349;
RA Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,
RA Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A.,
RA Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,
RA Ohno K.;
RT "NPC1 gene mutations in Japanese patients with Niemann-Pick disease
RT type C.";
RL Hum. Genet. 105:10-16(1999).
RN [9]
RP VARIANTS NPC1 GLN-958 AND ALA-1007.
RX MEDLINE=21313111; PubMed=11349231;
RA Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F.,
RA Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.;
RT "Niemann-Pick C variant detection by altered sphingolipid trafficking
RT and correlation with mutations within a specific domain of NPC1.";
RL Am. J. Hum. Genet. 68:1361-1372(2001).
RN [10]
RP VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.
RX MEDLINE=21313105; PubMed=11333381;
RA Millat G., Marcais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K.,
RA Wenger D.A., Ohno K., Vanier M.T.;
RT "Niemann-Pick C1 disease: correlations between NPC1 mutations, levels
RT of NPC1 protein, and phenotypes emphasize the functional significance
RT of the putative sterol-sensing domain and of the cysteine-rich
RT luminal loop.";
RL Am. J. Hum. Genet. 68:1373-1385(2001).
RN [11]
RP VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.
RX MEDLINE=21372069; PubMed=11479732;
RA Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T.,
RA Millat G.;
RT "Niemann-Pick type C disease: NPC1 mutations associated with severe
RT and mild cellular cholesterol trafficking alterations.";
RL Hum. Genet. 109:24-32(2001).
CC -!- FUNCTION: Involved in the intracellular trafficking of
CC cholesterol. May play a role in vesicular trafficking in glia, a
CC process that may be crucial for maintaining the structural and
CC functional integrity of nerve terminals.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Found in late
CC endosomes and lysosomes.

```
CC   -!- DOMAIN: A cysteine-rich N-terminal domain and a C-terminal domain
CC       containing a di-leucine motif necessary for lysosomal targeting
CC       are critical for mobilization of cholesterol from lysosomes.
CC   -!- PTM: Glycosylated.
CC   -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease
CC       type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lipid
CC       storage disorder, which affects particularly the brain, liver and
CC       spleen, and which is characterized by lysosomal accumulation of
CC       low density lipoprotein derived cholesterol. Clinical features
CC       include variable hepatosplenomegaly and severe progressive
CC       neurological dysfunction such as ataxia, dystonia and dementia.
CC       The age of onset can vary from infancy to late adulthood.
CC   -!- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease
CC       type D (NPD) [MIM:257250]; also known as Niemann-Pick disease
CC       without sphingomyelinase deficiency, or Nova Scotian type. Because
CC       of evidence from biochemical changes, lack of complementation, and
CC       linkage mapping to the same chromosome site, NPD and NPC1 are
CC       considered to be allelic disorders.
CC   -!- SIMILARITY: Belongs to the patched family.
CC   -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF002020; AAB63982.1; -.
DR   EMBL; AF157379; AAD48006.1; -.
DR   EMBL; AF157365; AAD48006.1; JOINED.
DR   EMBL; AF157366; AAD48006.1; JOINED.
DR   EMBL; AF157367; AAD48006.1; JOINED.
DR   EMBL; AF157368; AAD48006.1; JOINED.
DR   EMBL; AF157369; AAD48006.1; JOINED.
DR   EMBL; AF157370; AAD48006.1; JOINED.
DR   EMBL; AF157371; AAD48006.1; JOINED.
DR   EMBL; AF157372; AAD48006.1; JOINED.
DR   EMBL; AF157373; AAD48006.1; JOINED.
DR   EMBL; AF157374; AAD48006.1; JOINED.
DR   EMBL; AF157375; AAD48006.1; JOINED.
DR   EMBL; AF157376; AAD48006.1; JOINED.
DR   EMBL; AF157377; AAD48006.1; JOINED.
DR   EMBL; AF157378; AAD48006.1; JOINED.
DR   EMBL; AF338230; AAK25791.1; -.
DR   EMBL; AF123046; AAF28875.1; -.
DR   EMBL; AF123045; AAF28875.1; JOINED.
DR   Genew; HGNC:7897; NPC1.
DR   MIM; 607623; -.
DR   MIM; 257220; -.
DR   MIM; 257250; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005764; C:lysosome; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0005478; F:intracellular transporter activity; TAS.
DR   GO; GO:0015248; F:sterol transporter activity; TAS.
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DR   GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR   InterPro; IPR004765; NP_C_type.
DR   InterPro; IPR003392; Patched.
DR   InterPro; IPR000731; SSD_5TM.
DR   Pfam; PF02460; Patched; 1.
DR   TIGRFAMs; TIGR00917; 2A060601; 1.
DR   PROSITE; PS50156; SSD; 1.
KW   Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism;
KW   Disease mutation.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23   1278       NIEMANN-PICK C1 PROTEIN.
FT   TRANSMEM    270    290       POTENTIAL.
FT   TRANSMEM    351    371       POTENTIAL.
FT   TRANSMEM    622    642       POTENTIAL.
FT   TRANSMEM    655    675       POTENTIAL.
FT   TRANSMEM    678    698       POTENTIAL.
FT   TRANSMEM    760    780       POTENTIAL.
FT   TRANSMEM    833    853       POTENTIAL.
FT   TRANSMEM   1099   1119       POTENTIAL.
FT   TRANSMEM   1125   1145       POTENTIAL.
FT   TRANSMEM   1196   1216       POTENTIAL.
FT   TRANSMEM   1228   1248       POTENTIAL.
FT   DOMAIN      249    259       POLY-PRO.
FT   DOMAIN      620    785       SSD.
FT   SITE       1275   1278       DI-LEUCINE MOTIF.
FT   CARBOHYD     70     70       N-LINKED (GLCNAC. . .) (POTENTIAL).

  Query Match              9.6%;  Score 88.5;  DB 1;  Length 1278;
  Best Local Similarity   25.7%;  Pred. No. 12;
  Matches   39;  Conservative   25;  Mismatches   51;  Indels   37;  Gaps    7;

Qy         46 SVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 105
              ::||||   : :   : :  :   |       | ||  ::  | : ||||    ||  ||
Db        598 NLTISFTAERSIEDELNRESDSDVF------TVVISYAIMFLYISLALGH----IKSCRR 647

Qy        106 LFLVDD---------LVDSLKFAVLMWVFTYVGALFNGLTLLILALI----------SLF 146
              | |||          |:     |  : ||:|:|     |||::: :|          ::|
Db        648 L-LVDSKVSLGIAGILIVLSSVACSLGVFSYIGL---PLTLIVIEVIPFLVLAVGVDNIF 703

Qy        147 SIPVIYERHQ----VQIDHYLGLANKSVKDAM 174
                :   |:| :      :|  ||     |  :|
Db        704 ILVQAYQRDERLQGETLDQQLGRVLGEVAPSM 735


RESULT 13
MDLB_BUCBP
ID   MDLB_BUCBP     STANDARD;      PRT;   578 AA.
AC   Q89A96;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Multidrug resistance-like ATP-binding protein mdlB.
GN   MDLB OR BBP424.
OS   Buchnera aphidicola (subsp. Baizongia pistaciae).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Buchnera.
OX   NCBI_TaxID=135842;
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RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426901; PubMed=12522265;
RA   Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,
RA   Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
RA   Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
RT   "Reductive genome evolution in Buchnera aphidicola.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE014017; AAO27134.1; -.
DR   InterPro; IPR001140; ABC_TM_transpt.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   PROSITE; PS50929; ABC_TM1F; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Transport; Transmembrane; Complete proteome.
FT   TRANSMEM     26     46       POTENTIAL.
FT   TRANSMEM     59     79       POTENTIAL.
FT   TRANSMEM    143    163       POTENTIAL.
FT   TRANSMEM    166    186       POTENTIAL.
FT   TRANSMEM    196    216       POTENTIAL.
FT   TRANSMEM    260    280       POTENTIAL.
FT   DOMAIN      339    573       ABC TRANSPORTER.
FT   NP_BIND     373    380       ATP (POTENTIAL).
SQ   SEQUENCE   578 AA;  66827 MW;  3B84848CE196ADF7 CRC64;

  Query Match              9.4%;  Score 86.5;  DB 1;  Length 578;
  Best Local Similarity   19.9%;  Pred. No. 7.8;
  Matches   43;  Conservative   46;  Mismatches   72;  Indels   55;  Gaps   10;

Qy          1 SVVD-------LLYWRDIKKTGVVFGASLFLLLSL--------------------TV-FS 32
                :|:|       |||:    |  :: | :| |  |:                      || :|
Db          3 NVIDFWPTLKRLLYYGTNVKKYLILGFTLLLFSSIFEVLNPILISCFIKHYFINNTVNYS 62

Qy         33 IVSVTAYIALALLSVTISF-------RIYKGVIQA----IQKSDEGHPFRAYLESEVAIS 81
              :  :| |: | :|:  :::       :|   |||     :  |    | : : :  :
Db         63 LKIITYYLILQILAAILNYHQNIIFNKISLTVIQKLRYDVMSSTLQLPIKMFDQRPIG-- 120

Qy         82 EELVQKYSNSALGHVNSTIKEL-----RRLF--LVDDLVDSLKFAVLMWVFTYVGALFNG 134
               : : : :|        |||||     : ||  ::  |:  :   :| |    : ::
Db        121 -QFISRITND-----TETIKELYDTVIKSLFQNIILILITLITMFILEWRMACIASIIFP 174

Qy        135 LTLLILALISLFSIPVIYERHQVQIDHYLGLANKSV 170
              : |:|: |   || |::  : :| | :   : |: :
Db        175 IALIIMLLYQYFSKPIL-RKIKVYIANIYNIFNEII 209
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RESULT 14
Y015_MYCGE
ID   Y015_MYCGE     STANDARD;      PRT;   589 AA.
AC   P47261;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical ABC transporter ATP-binding protein MG015.
GN   MG015.
OS   Mycoplasma genitalium.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=96026346; PubMed=7569993;
RA   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA   Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA   Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA   Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA   Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA   Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT   "The minimal gene complement of Mycoplasma genitalium.";
RL   Science 270:397-403(1995).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: Belongs to the ABC transporter family. MsbA subfamily.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U39680; AAC71231.1; -.
DR   PIR; F64201; F64201.
DR   HSSP; P13569; 1NBD.
DR   TIGR; MG015; -.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR001140; ABC_TM_transpt.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00664; ABC_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS50929; ABC_TM1F; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   Hypothetical protein; ATP-binding; Transport; Transmembrane;
KW   Complete proteome.
FT   TRANSMEM      9     29       POTENTIAL.
FT   TRANSMEM     66     86       POTENTIAL.
FT   TRANSMEM    161    181       POTENTIAL.
FT   TRANSMEM    251    271       POTENTIAL.
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FT   TRANSMEM    280    300       POTENTIAL.
FT   TRANSMEM    303    323       POTENTIAL.
FT   NP_BIND     385    392       ATP (POTENTIAL).
SQ   SEQUENCE   589 AA;  66126 MW;  0EA6A816DD3A3CC9 CRC64;

  Query Match              9.3%;  Score 86;  DB 1;  Length 589;
  Best Local Similarity   22.7%;  Pred. No. 8.8;
  Matches   45;  Conservative   40;  Mismatches   71;  Indels   42;  Gaps    7;

Qy          3 VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQ 62
              || :|        :::  :| : : ||   ||||| ::| ||: |    : | | |:  |
Db         48 VDSIY-------SLIYPTNLNVFIRLT---IVSVTVFVAYALIFVFNVAQNYVG-IKLYQ 96

Qy         63 KSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLF------LVDDLVDSL 116
              ::     ::|||: :   :     : :   :  : : :  :  ||       :  | : |
Db         97 QTCATLRWKAYLKMQSMSTSFFDTQNNGDLMSRLTNDMYNIDNLFTQAGGQAIQSLFNIL 156

Qy        117 KFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYER----HQVQ-------------- 158
                :||::: : | ||   ::| ||| :  ||   : :      |||
Db        157 TTSVLIFLLSPVIAL---ISLSILATLITFSFAFLKKSKTSYSQVQNNLGDMSGYIEEVL 213

Qy        159 ----IDHYLGLANKSVKD 172
                   : | | |    :||
Db        214 TNHKVVHVLKLQEIMIKD 231


RESULT 15
YBZ7_YEAST
ID   YBZ7_YEAST     STANDARD;      PRT;   296 AA.
AC   P38279;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   Hypothetical 33.5 kDa protein in MRPS9-YSW1 intergenic region.
GN   YBR147W OR YBR1124.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RA   Entian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
RA   Niegemann E., Schenk-Groeninger R., Servos J., Wehner E.,
RA   Wolter R., Brendel M., Bauer J., Braun H., Dern K., Duesterhus S.,
RA   Gruenbein R., Hedges D., Kiesau P., Korol S., Krems B., Proft M.,
RA   Siegers K., Baur A., Boles E., Miosga T.,
RA   Schaaff-Gerstenschlaeger I., Zimmermann F.K.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: SOME, TO S.POMBE SPAC2E12.03C AND SPAC17C9.10.
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CC   ------------------------------------------------------------------------
DR   EMBL; Z36016; CAA85105.1; -.
DR   PIR; S46018; S46018.
DR   GermOnline; 138690; -.
DR   SGD; S0000351; YBR147W.
DR   InterPro; IPR006603; CTNS.
DR   Pfam; PF04193; PQ-loop; 2.
DR   SMART; SM00679; CTNS; 2.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM     13     33       POTENTIAL.
FT   TRANSMEM     45     65       POTENTIAL.
FT   TRANSMEM     69     89       POTENTIAL.
FT   TRANSMEM    164    184       POTENTIAL.
FT   TRANSMEM    200    220       POTENTIAL.
FT   TRANSMEM    239    259       POTENTIAL.
FT   TRANSMEM    263    283       POTENTIAL.
SQ   SEQUENCE   296 AA;  33496 MW;  50D65896A1BAFB43 CRC64;

  Query Match             9.2%;  Score 85.5;  DB 1;  Length 296;
  Best Local Similarity   29.3%;  Pred. No. 4.7;
  Matches   41;  Conservative   17;  Mismatches   55;  Indels   27;  Gaps    7;

Qy         17 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIY----KGVIQAIQKS-DEGH--- 68
              | || :  ||     ::: : ||  || | : |    |    | ::| ::|: |  |
Db         61 VMGAMMQNLLP----TMIILAAYYTLADLILLIQCMWYDKEKKSILQEVKKNVDPVHLPP 116

Qy         69 -----------PFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDS-- 115
                         |  |      | ||  | ||:  ||     :|| |  |  | |: |
Db        117 ANPINETVLQDVFNEYEPLLPRIEEEDSQSYSSLELGR-TIVVKE-RENFFNDFLIVSGV 174

Qy        116 LKFAVLMWVFTYVGALFNGL 135
              |   :| |  :|   | ||:
Db        175 LIAGILSWYISYCSGLDNGI 194


Search completed: September 29, 2004, 18:14:38
Job time : 3.70944 secs
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